

REMARKS

The Specification has been amended to correct erroneous sequence identification numbers and include sequence identification numbers which were omitted at the time of filing.

Attached hereto is a marked-up version of the changes made to the specification by the current amendment. The attached page is captioned "Version with markings to show changes made.".

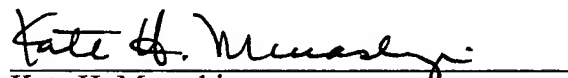
The undersigned hereby states that the compact disc copy of the Sequence Listing and the computer readable form copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.825(a) and (b), respectively, are the same and contain no new matter. Accordingly, entry of the Sequence Listing into the above-captioned case is respectfully requested.

In the unlikely event that the patent office determines that extensions and/or other relief is required, applicant petition for any required relief including extensions of time and authorize the assistant commissioner to charge the cost of such petitions and/or fees due to our deposit account no. 03-1952 under order no. 511582002420. The assistant commissioner is not authorized to charge the cost of the issue fee to the deposit account.

Respectfully submitted,

Dated: May 20, 2002

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

The paragraph beginning at page 7, line 21, has been amended as follows:

Figure 1. 101P3A11 SSH sequence (SEQ ID NO:2960). The 101P3A11 SSH sequence.

The paragraph beginning at page 7, line 22, has been amended as follows:

Figures 2A-2D. The cDNA (SEQ ID. NO. :2961) and amino acid sequence (SEQ ID. NO. :2962) of 101P3A11. The start methionine is underlined. The open reading frame extends from nucleic acid 133 to 1086 including the stop codon (the codon for the initial M is omitted as the shorter peptide has a more favorable Kozak sequence).

The paragraph beginning at page 7, line 26, has been amended as follows:

Figure 3. Amino acid sequence of 101P3A11 (SEQ ID. NO. :piece of 2962). The 101P3A11 protein has 317 amino acids.

The paragraph beginning at page 7, line 28, has been amended as followsh:

Figure 4. Alignment of 101P3A11 (Sbjct) (SEQ ID NO: 2964) with mouse olfactory receptor S25 (Query.) (SEQ ID NO: 2963) The transmembrane regions of 101P3A11 and mouse olfactory receptor S25 (ORS25) predicted using the TMHMM algorithm are highlighted in gray. The amino acids of ORS25 predicted (Floriano, W.B., et al, 2000, Proc. Natl. Acad. Sci., USA, 97:10712-10716) to be involved in binding of the ligand hexanol and/or involved in the formation of the ligand binding pocket are italicized and bolded in the Figure, and are: Leu 131, Val 134, Val 135, Gly 138, Thr139, Ser 193, Ser 197, Phe 225, Ala 230, Ile 231, Gly 234, Thr 284, Phe 287, Gln 300, Lys 302.

The paragraph beginning at page 11, line 31, has been amended as follows:

Figure 23. Alignment of 101P3A11-PHOR-1 (Phor) (SEQ ID NO: 2965) with the rat (SEQ ID NO: 2966) GPCR RA1C (gi|3420759). Identities = 179/299 (59%), Positives = 231/299 (76%), Gaps = 1/299 (0%).

The paragraph beginning at page 12, line 1, has been amended as follows:

Figure 24. Alignment of 101P3A11-PHOR-1 (Phor) (SEQ ID NO: 2967) with the human prostate specific GPCR (SEQ ID NO: 2968) (gi|13540539). Identities = 179/299 (59%), Positives = 233/299 (77%), Gaps = 1/299 (0%).

The paragraph beginning at page 12, line 3, has been amended as follows:

Figure 25. Alignment of 101P3A11-PHOR-1 (Phor) (SEQ ID NO: 2969) with human olfactory receptor 5II12, HOR5 (SEQ ID NO: 2970) (gi|14423836). Identities = 163/304 (53%), Positives = 214/304 (69%), Gaps = 1/304 (0%).

The paragraph beginning at page 36, line 20, has been amended as follows:

Also, different MHC class I molecules prefer a different length of ligands. For example, SYFPEITHI offers predictions for H2-Kb octamers, HLA-A*0201 nonamers and decamers, or HLA-B8 octamers and nonamers. The maximal scores vary between different MHC alleles. Therefore, one can include known ligands/epitopes in order to have an approximation of the scoring. For example, the maximal score for HLA-A*0201 peptides is 36. The well-known epitope GILGFVFTL (SEQ ID NO: 1401) derived from the influenza A matrix protein scores 30. All predicted MHC class II ligands are 15mers, consisting of three N-terminal flanking residues, the nonamer core sequence located within the binding groove, and three C-terminal flanking residues. Thus, anchor residue P1 appears in position 4 of the peptides predicted with "SYFPEITHI".

The paragraph beginning at page 37, line 25, has been amended as follows:

In an embodiment described in the examples that follow, 101P3A11 can be conveniently expressed in cells (such as 293T cells) transfected with a commercially available expression vector such as a CMV-driven expression vector encoding 101P3A11 with a C-terminal 6XHis (SEQ ID NO: 1402) and MYC tag (pcDNA3.1/mycHIS, Invitrogen or Tag5, GenHunter Corporation, Nashville TN). The Tag5 vector provides an IgGK secretion signal that can be used to facilitate the production of a secreted 101P3A11 protein in transfected cells. The secreted HIS-tagged 101P3A11 in the culture media can be purified, e.g., using a nickel column using standard techniques.

The paragraph beginning at page 70, line 3, has been amended as follows:

In certain embodiments, the T helper peptide is one that is recognized by T helper cells present in a majority of a genetically diverse population. This can be accomplished by selecting peptides that bind to many, most, or all of the HLA class II molecules. Examples of such amino acid bind many HLA Class II molecules include sequences from antigens such as tetanus toxoid at positions 830-843 (QYIKANSKFIGITE; [SEQ ID NO: 710] (SEQ ID NO: 1403), *Plasmodium falciparum* circumsporozoite (CS) protein at positions 378-398 (DIEKKIAKMEKASSVFNVVNS; [SEQ ID NO: 711] (SEQ ID NO: 1404), and *Streptococcus* 18kD protein at positions 116-131 (GAVDSILGGVATYGAA; [SEQ ID NO: 712] (SEQ ID NO: 1405)). Other examples include peptides bearing a DR 1-4-7 supermotif, or either of the DR3 motifs.

The paragraph beginning at page 70, line 11, has been amended as follows:

Alternatively, it is possible to prepare synthetic peptides capable of stimulating T helper lymphocytes, in a loosely HLA-restricted fashion, using amino acid sequences not found in nature (*see, e.g.*, PCT publication WO 95/07707). These synthetic compounds called Pan-DR-binding epitopes (*e.g.*, PADRE™, Epimmune, Inc., San Diego, CA) are designed to most preferably bind most HLA-DR (human HLA class II) molecules. For instance, a pan-DR-binding epitope peptide having the formula: aKXVAAWTLKAAa [SEQ ID NO: 713] (SEQ ID NO: 1406), where "X" is either cyclohexylalanine, phenylalanine, or tyrosine, and a is either D-alanine or L-alanine, has been found to bind to most HLA-DR alleles, and to stimulate the response of T helper lymphocytes from most individuals, regardless of their HLA type. An alternative of a pan-DR binding epitope comprises all "L" natural amino acids and can be provided in the form of nucleic acids that encode the epitope.

The paragraph beginning at page 80, line 16, has been amended as follows:

Single chain antibodies comprise the variable domains of the heavy and light chain joined by a flexible linker polypeptide, and are expressed as a single polypeptide. Optionally, single chain antibodies are expressed as a single chain variable region fragment joined to the light chain constant region. Well-known intracellular trafficking signals are engineered into recombinant

polynucleotide vectors encoding such single chain antibodies in order to precisely target the intrabody to the desired intracellular compartment. For example, intrabodies targeted to the endoplasmic reticulum (ER) are engineered to incorporate a leader peptide and, optionally, a C-terminal ER retention signal, such as the KDEL (SEQ ID NO: 1407) amino acid motif.

Intrabodies intended to exert activity in the nucleus are engineered to include a nuclear localization signal. Lipid moieties are joined to intrabodies in order to tether the intrabody to the cytosolic side of the plasma membrane. Intrabodies can also be targeted to exert function in the cytosol. For example, cytosolic intrabodies are used to sequester factors within the cytosol, thereby preventing them from being transported to their natural cellular destination.

The paragraph beginning at page 86, line 29, has been amended as follows:

pGEX Constructs: To generate recombinant 101P3A11 proteins in bacteria that are fused to the Glutathione S-transferase (GST) protein, all or parts of the 101P3A11 cDNA protein coding sequence are fused to the GST gene by cloning into pGEX-6P-1 or any other GST- fusion vector of the pGEX family (Amersham Pharmacia Biotech, Piscataway, NJ). These constructs allow controlled expression of recombinant 101P3A11 protein sequences with GST fused at the amino-terminus and a six histidine epitope (6X His) (SEQ ID NO: 1402) at the carboxyl-terminus. The GST and 6X His tags permit purification of the recombinant fusion protein from induced bacteria with the appropriate affinity matrix and allow recognition of the fusion protein with anti-GST and anti-His antibodies. The 6X His tag (SEQ ID NO: 1402) is generated by adding 6 histidine (SEQ ID NO: 1402) codons to the cloning primer at the 3' end, e.g., of the open reading frame (ORF). A proteolytic cleavage site, such as the PreScissionTM recognition site in pGEX-6P-1, can be employed that permits cleavage of the GST tag from 101P3A11-related protein. The ampicillin resistance gene and pBR322 origin permit selection and maintenance of the pGEX plasmids in *E. coli*. In one embodiment, amino acids 86-317 are cloned into the pGEX-2T expression vector, the protein is expressed and purified.

The paragraph beginning at page 87, line 8, has been amended as follows:

pMAL Constructs: To generate, in bacteria, recombinant 101P3A11 proteins that are fused to maltose-binding protein (MBP), all or parts of the 101P3A11 cDNA protein coding sequence are fused to the MBP gene by cloning into the pMAL-c2X and pMAL-p2X vectors

(New England Biolabs, Beverly, MA). These constructs allow controlled expression of recombinant 101P3A11 protein sequences with MBP fused at the amino-terminus and a 6X His (SEQ ID NO: 1402) epitope tag at the carboxyl-terminus. The MBP and 6X His tags (SEQ ID NO: 1402) permit purification of the recombinant protein from induced bacteria with the appropriate affinity matrix and allow recognition of the fusion protein with anti-MBP and anti-His antibodies. The 6X His (SEQ ID NO: 1402) epitope tag is generated by adding 6 histidine (SEQ ID NO: 1402) codons to the 3' cloning primer. A Factor Xa recognition site permits cleavage of the pMAL tag from 101P3A11. The pMAL-c2X and pMAL-p2X vectors are optimized to express the recombinant protein in the cytoplasm or periplasm respectively. Periplasm expression enhances folding of proteins with disulfide bonds. In one embodiment, amino acids 86-310 is cloned into the pMAL-c2X expression vector, the protein is expressed and purified.

The paragraph beginning at page 87, line 20, has been amended as follows:

pET Constructs: To express 101P3A11 in bacterial cells, all or parts of the 101P3A11 cDNA protein coding sequence are cloned into the pET family of vectors (Novagen, Madison, WI). These vectors allow tightly controlled expression of recombinant 101P3A11 protein in bacteria with and without fusion to proteins that enhance solubility, such as NusA and thioredoxin (Trx), and epitope tags, such as 6X His (SEQ ID NO: 1402) and S-Tag™ that aid purification and detection of the recombinant protein. For example, constructs are made utilizing pET NusA fusion system 43.1 such that regions of the 101P3A11 protein are expressed as amino-terminal fusions to NusA.

The paragraph beginning at page 88, line 19, has been amended as follows:

pcDNA4/HisMax Constructs: To express 101P3A11 in mammalian cells, the 101P3A11 ORF was cloned into pcDNA4/HisMax Version A (Invitrogen, Carlsbad, CA). Protein expression is driven from the cytomegalovirus (CMV) promoter and the SP16 translational enhancer. The recombinant protein has Xpress™ and six histidine (6X His) (SEQ ID NO: 1402) epitopes fused to the amino-terminus. The pcDNA4/HisMax vector also contains the bovine growth hormone (BGH) polyadenylation signal and transcription termination sequence to enhance mRNA stability along with the SV40 origin for episomal replication and

simple vector rescue in cell lines expressing the large T antigen. The Zeocin resistance gene allows for selection of mammalian cells expressing the protein and the ampicillin resistance gene and ColE1 origin permits selection and maintenance of the plasmid in *E. coli*.

The paragraph beginning at page 88, line 28, has been amended as follows:

pcDNA3.1/MycHis Constructs: To express 101P3A11 in mammalian cells, the 101P3A11 ORF, with a consensus Kozak translation initiation site, was cloned into pcDNA3.1/MycHis Version A (Invitrogen, Carlsbad, CA). Protein expression is driven from the cytomegalovirus (CMV) promoter. The recombinant proteins have the myc epitope and 6X His (SEQ ID NO: 1402) epitope fused to the carboxyl-terminus. The pcDNA3.1/MycHis vector also contains the bovine growth hormone (BGH) polyadenylation signal and transcription termination sequence to enhance mRNA stability, along with the SV40 origin for episomal replication and simple vector rescue in cell lines expressing the large T antigen. The Neomycin resistance gene can be used, as it allows for selection of mammalian cells expressing the protein and the ampicillin resistance gene and ColE1 origin permits selection and maintenance of the plasmid in *E. coli*.

The paragraph beginning at page 89, line 16, has been amended as follows:

PAPtag: The 101P3A11 ORF, or portions thereof, of 101P3A11 are cloned into pAPtag-5 (GenHunter Corp. Nashville, TN). This construct generates an alkaline phosphatase fusion at the carboxyl-terminus of the 101P3A11 proteins while fusing the IgGκ signal sequence to the amino-terminus. Constructs are also generated in which alkaline phosphatase with an amino-terminal IgGκ signal sequence is fused to the amino-terminus of 101P3A11 proteins. The resulting recombinant 101P3A11 proteins are optimized for secretion into the media of transfected mammalian cells and can be used to identify proteins such as ligands or receptors that interact with the 101P3A11 proteins. Protein expression is driven from the CMV promoter and the recombinant proteins also contain myc and 6X His (SEQ ID NO: 1402) epitopes fused at the carboxyl-terminus that facilitates detection and purification. The Zeocin resistance gene present in the vector allows for selection of mammalian cells expressing the recombinant protein and the ampicillin resistance gene permits selection of the plasmid in *E. coli*.

The paragraph beginning at page 89, line 27, has been amended as follows:

ptag5: The 101P3A11 ORF, or portions thereof, of 101P3A11 are cloned into pTag-5. This vector is similar to pAptag but without the alkaline phosphatase fusion. This construct generated 101P3A11 protein with an amino-terminal IgGκ signal sequence and myc and 6X His (SEQ ID NO: 1402) epitope tags at the carboxyl-terminus that facilitate detection and affinity purification. The resulting recombinant 101P3A11 protein was optimized for secretion into the media of transfected mammalian cells, and was used as immunogen or ligand to identify proteins such as ligands or receptors that interact with the 101P3A11 proteins. Protein expression is driven from the CMV promoter. The Zeocin resistance gene present in the vector allows for selection of mammalian cells expressing the protein, and the ampicillin resistance gene permits selection of the plasmid in *E. coli*.

The paragraph beginning at page 90, line 30, has been amended as follows:

Additional pSRα constructs are made that fuse an epitope tag such as the FLAGTM tag to the carboxyl-terminus of 101P3A11 sequences to allow detection using anti-Flag antibodies. For example, the FLAGTM sequence 5' gat tac aag gat gac gac gat aag 3' (SEQ ID NO: 1408) is added to cloning primer at the 3' end of the ORF. Additional pSRα constructs are made to produce both amino-terminal and carboxyl-terminal GFP and myc/6X His (SEQ ID NO: 1402) fusion proteins of the full-length 101P3A11 proteins.

The paragraph beginning at page 141, line 31, has been amended as follows:

The generation of anti-101P3A11 polyclonal Ab (pAb) using an amino-terminal peptide encoding amino acids 1-14 (MVDPNGNESSATYF; [SEQ ID NO:YY] (SEQ ID NO: 1409)) as antigen was reported in our Priority Application. The effect of this antibody on 101P3A11 mediated ERK phosphorylation (Figure 38) and cAMP accumulation (Figure 39) was determined. 293T cells were transfected with control or 101P3A11 cDNA. Cells were allowed to rest overnight, and treated with anti-101P3A11 or control Ab in the presence of 0.5% or 10% FBS. Cells were lysed and analyzed by Western blotting with anti-Phospho-ERK and anti-ERK mAb. Figure 38 shows that expression of 101P3A11 induces ERK phosphorylation in cells treated with 0.5 or 10% FBS. Anti-101P3A11 pAb reduced the phosphorylation of ERK in

293T-101P3A11 cells treated with 0.5% FBS. The ERK overlay demonstrated equal loading, supporting the specificity of this data.

Table XIX, beginning at page 186, has been amended as follows:

Table XIX: Motifs and Post-translational Modifications of 101P3A11

N-glycosylation site

Number of matches: 3

- 1 7-10 NESS (SEQ ID NO: 1410)
- 2 44-47 NLTI (SEQ ID NO: 1411)
- 3 90-93 NSTT (SEQ ID NO: 1412)

cAMP- and cGMP-dependent protein kinase phosphorylation site
268-271 RRDS (SEQ ID NO: 1413)

Protein kinase C phosphorylation site
266-268 SKR

Casein kinase II phosphorylation site

Number of matches: 3

- 1 56-59 SLHE (SEQ ID NO: 1414)
- 2 69-72 SGID (SEQ ID NO: 1415)
- 3 110-113 SGME (SEQ ID NO: 1416)

N-myristoylation site

Number of matches: 4

- 1 6-11 GNESSA (SEQ ID NO: 1417)
- 2 21-26 GLEEAQ (SEQ ID NO: 1418)
- 3 111-116 GMESTV (SEQ ID NO: 1419)
- 4 240-245 GTCVSH (SEQ ID NO: 1420)

G-protein coupled receptors family 1 signature
112-128 MESTVLLAMAFDRYVAI (SEQ ID NO: 1421)

Table XXI, beginning at page 190, line 1, has been amended as follows:

Table XXI: Nucleotide sequence of the splice variant (SEQ ID NO: 1422)

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1 CACATTCCTT CCATACGGTT GAGCCTCTAC CTGCCTGGTG CTGGTCACAG TTCAGCTTCT
61 TCATGATGGT GGATCCCAAT GGCAATGAAT CCAGTGCTAC ATACTTCATC CTAATAGGCC
121 TCCCTGGTTT AGAAGAGGCT CAGTTCTGGT TGGCCTCCCA TTGTGCTCCC TCTANCTATG
181 CTGTGCTAGT AATTGACAAT CATCTACATG TGCGGACGAG CACGNCGCNG AGCCCNGTAT
241 NATTCTGCNG CTTCAGCATG ACACCCTNCA GTCTCAGCCA AAGNGCATCT CNGTCAATCA
301 NACACNTGAG CTGTCGTACG AGTTGCATCA TCCTANGGCA GGATCAATGT GCGGNAGGCN

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361 TGACGCAGTG CACGTACCAT GGCAGCAAGA CAGGGCCGGT ACAAATGGGG GCGAGNCGGG
421 GTGAAGATGN ACCCTCGGGT CANAGAGTGC CTCTGCGCCA AAACCTCCAT CATGNNAACA
481 GNGTATAACG GCGNAGAATC GGNNANGCGC AAGGCTAAGG AAANNCCCCA NNCNGGTACT
541 TTAACCCNGC AAANGGCANC NAAACGGGNG GGTNANTGAA CAAGGAAGGN NTGNAACTGG
601 GCCAAAACGG GNTGGGCAAN NNAAGGACTC ATGGGNCCAA GGGACGGNAA AAGGGGNAAN
661 CGGGGCGAAA TGNNAAAAAC CGGGNCCCGG GGAANAANGA AGGGGAANAN GNGTGAAGGA
721 CNGGGTTCAA GGGAAAAGNA AAACCANGGG NNAGAAACCN TTCNAANGGC CCGGGNANGA
781 AAGGAANTNN GNNNGGNGAA AAAATCNAAA AAAAGCNGNG GCNNAAAAAN GGGGGGAANN
841 NAAANACCNN GGNCGNNAAA AAACNNAANG NGGGGGGANT ANACACGGAA ANNNANGGGC
901 GNNNAAGGGA AATAANNCGG GAACNAAAGN GCAAACCGNA CGGNAGGAAC GAAACCCACC
961 GGAGNCGCNN AACGCCNNNC NNANCCCGAG CNGAGGTNG

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Table XXII, beginning at page 190, line 38, has been amended as follows:

Table XXII: Nucleotide sequence alignment of 101P3A11 with the splice variant.

Score = 337 bits (175), Expect = 4e-89

Identities = 215/223 (96%), Gaps = 6/223 (2%)

Strand = Plus / Plus

101P3A11: 68 cacattccttcatacgggttgagcctctacctgctggtgctggtcacagttcagcttct 127
(SEQ ID NO: 1423)

Variant : 1 cacattccttcatacgggttgagcctctacctgctggtgctggtcacagttcagcttct 60
(SEQ ID NO: 1424)

101P3A11: 128 tcatgatggtggatcccaatggcaatgaatccagtgtacatacttcacctaataaggcc 187

Variant : 61 tcatgatggtggatcccaatggcaatgaatccagtgtacatacttcacctaataaggcc 120

101P3A11: 188 tccctggtttagaagaggctcagttctggttgcccttccattgtgctccctctacctta 247

Variant : 121 tccctggtttagaagaggctcagttctggttgcc-tccattgtgctccctctanct-- 177

101P3A11: 248 ttgctgtgctaggtaacttgacaatcatctacattgtgcggac 290

Variant : 178 atgctgtgcta-gtaa-ttgacaatcatctaca-tgtgcggac 217

Table XXIII, beginning at page 191, line 8, has been amended as follows:

Table XXIII: Longest single amino acid sequence alignment of 101P3A11 and the splice variant.

Score = 134 bits (287), Expect (2) = 3e-29

Identities = 51/51 (100%)

Frame = +1 / +3

101P3A11: 70 HSFHTVEPLPAWCWSQFSFFMMVDPNGNESSATYFILIGLPGLEEAQFWLA 222
 (SEQ ID NO: 1425)
 HSFHTVEPLPAWCWSQFSFFMMVDPNGNESSATYFILIGLPGLEEAQFWLA
 Variant : 3 HSFHTVEPLPAWCWSQFSFFMMVDPNGNESSATYFILIGLPGLEEAQFWLA 155
 (SEQ ID NO: 1426)

Table XXIV, beginning at page 191, line 16, has been amended as follows:

Table XXIV: Peptide sequences from the translation of the nucleotide sequence of the splice variant .

Open reading frame	Amino acid sequences
Frame 1 (SEQ ID NO: 1427)	HIPSIRLSLYLPGAGHSSASS*WWIPMAMNPVLHTSS**ASLV*KRLSSGWPPIVLPLXM LC**LTIIYMCGRARRXAXYXSAASA*HPXVSAKXHLXQSXT*AVVRVASSXGRINVRXA *RSARTMAARQGRYKWXGVMXPRVXECLCAKTSIMXTXNGXESXXRKAKEXPXXGT LTXXQXAXKRXGX*TRXXXNWAKTGWAXXGLMGPDRDGKRGXRGEMXKTGXRGXXKGXXXEG XGSREKXNXGXETXXXARXXXKEXXXXXKSKSXGXKXGGXXXPXXXKNXXXGXTRKXXG XXGK*XGNXXANRTXGKTGTXAXRXXXPEXX
Frame 2 (SEQ ID NO: 1428)	TFLPYG*ASTCLVLVTQLLHDGGSQWQ*IQCYILHPNRPPWFRRGSVLVGLPLCSLXLC CASN*QSSTCADEHXAEPXXILXLQHDTLQSQPKXISVNXTXELSYELHHPXAGSMCGRX DAHVHPWQQDRAGTNGGEXG*RTLGSXSASAPKPPSXXQXITAXNRXXARLRKXPXXVL *PXKXXXNGXVXEQGRXXTGPKRXGQXKDSWXQGTXXKXXGAKXXKPGPGEXXRGXXVKD XVQGXKTXGXKPFXXPGXERXXXXXKNXXKAXAXKXGEXKXXGRXKTXXGXXHGXXXA XKGNXXGTXQTXXRERNPPEXXNAXXXPSXG
Frame 3 (SEQ ID NO: 1429)	HSFHTVEPLPAWCWSQFSFFMMVDPNGNESSATYFILIGLPGLEEAQFWLASHCAPSXYA VLVIDNHLHVRTSTXXSPVXFCXFSMTXSLXSQXASXSIXHXSCRTSCIILXQDQCAXGX TQCTYHGSKTGPVQMGAXRGEDXPSGXRVPLRQNLHXXNXV*RRRIGXAQG*GXXQXXYF NPAXGXXTGXXNKEGXXLGQNGXGXXRTHGXKGRXKGRXXGRNXXKNRXPXXEGEXX*RT GFKGXKXPXXRNXXSGPGXKGGXXGEXKIXKXXXXXKGGXXTXXXXKXXGXXTEXXGR XREIXREXKXKPGXGRNETHRXRXTPXXXRAEV

Note: Frame 3 gives the longest subsequence that is identical with 101P3A11 amino acid sequence. In this Table each (*) indicates the product of a single stop codon, and 'X' indicates a single unknown amino acid.

Table XXVI, beginning at page 193, line 1, has been amended as follows:

Table XXVI:

HLA Class I Nonamers (SEQ ID NOS 1430-1462, respectively in order of appearance)

HLA-A1 nonomers										
	Pos	1	2	3	4	5	6	7	8	9 score
1	245	H	V	C	A	V	F	I	F	Y 24
2	29	L	A	F	P	L	C	S	L	Y 21
3	41	V	L	G	N	L	T	I	I	Y 21
4	285	P	P	V	L	N	P	I	V	Y 20
5	111	G	M	E	S	T	V	L	L	A 19
6	117	L	L	A	M	A	F	D	R	Y 19
7	172	R	S	N	I	L	S	H	S	Y 19
8	192	D	D	I	R	V	N	V	V	Y 19
9	212	D	S	L	L	I	S	F	S	Y 19
10	57	L	H	E	P	M	Y	I	F	L 18
11	22	L	E	E	A	Q	F	W	L	A 17
12	9	S	S	A	T	Y	F	I	L	I 16
13	52	R	T	E	H	S	L	H	E	P 16
14	54	E	H	S	L	H	E	P	M	Y 16

HLA-A1 nonomers

	Pos	1	2	3	4	5	6	7	8	9	score
15	78	S	<u>S</u>	M	P	K	M	<u>L</u>	A	I	16
16	95	Q	<u>F</u>	D	A	C	L	<u>L</u>	Q	I	16
17	159	A	<u>P</u>	L	P	V	F	<u>I</u>	K	Q	16
18	183	H	<u>Q</u>	D	V	M	K	<u>L</u>	A	C	16
19	1	M	<u>V</u>	D	P	N	G	<u>N</u>	E	S	15
20	5	N	<u>G</u>	N	E	S	S	<u>A</u>	T	Y	15
21	210	G	<u>L</u>	D	S	L	L	<u>I</u>	S	F	15
22	273	L	<u>P</u>	V	I	L	A	<u>N</u>	I	Y	15
23	271	S	<u>P</u>	L	P	V	I	<u>L</u>	A	N	14
24	91	S	<u>T</u>	T	I	Q	F	<u>D</u>	A	C	13
25	121	A	<u>F</u>	D	R	Y	V	<u>A</u>	I	C	13
26	138	L	<u>T</u>	L	P	R	V	<u>T</u>	K	I	13
27	218	F	<u>S</u>	Y	L	L	I	<u>L</u>	K	T	13
28	282	L	<u>L</u>	V	P	P	V	<u>L</u>	N	P	13
29	190	A	<u>C</u>	D	D	I	R	<u>V</u>	N	V	12
30	191	C	<u>D</u>	D	I	R	V	<u>N</u>	V	V	12
31	231	T	<u>R</u>	E	A	Q	A	<u>K</u>	A	F	12
32	268	R	<u>R</u>	D	S	P	L	<u>P</u>	V	I	12
33	270	D	<u>S</u>	P	L	P	V	<u>I</u>	L	A	12

HLA-A*0201 nonomers (SEQ ID
NOS 1463-1569, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	287	V	L	N	P	I	<u>V</u>	Y	G	V	30
2	14	F	I	L	I	G	<u>L</u>	P	G	L	29
3	28	W	L	A	F	P	<u>L</u>	C	S	L	28
4	37	Y	L	I	A	V	<u>L</u>	G	N	L	28
5	222	L	I	L	K	T	<u>V</u>	L	G	L	28
6	66	C	M	L	S	G	<u>I</u>	D	I	L	26
7	108	S	L	S	G	M	<u>E</u>	S	T	V	26
8	181	C	L	H	Q	D	<u>V</u>	M	K	L	26
9	201	G	L	I	V	I	<u>I</u>	S	A	I	26
10	214	L	L	I	S	F	<u>S</u>	Y	L	L	26
11	275	V	I	L	A	N	<u>I</u>	Y	L	L	26
12	157	L	M	A	P	L	<u>P</u>	V	F	I	25
13	220	Y	L	L	I	L	<u>K</u>	T	V	L	25
14	276	I	L	A	N	I	<u>Y</u>	L	L	V	25
15	279	N	I	Y	L	L	<u>V</u>	P	P	V	25
16	138	L	T	L	P	R	<u>V</u>	T	K	I	24
17	213	S	L	L	I	S	<u>F</u>	S	Y	L	24
18	49	Y	I	V	R	T	<u>E</u>	H	S	L	23
19	143	V	T	K	I	G	<u>V</u>	A	A	V	23
20	188	K	L	A	C	D	<u>D</u>	I	R	V	23
21	198	V	V	Y	G	L	<u>I</u>	V	I	I	23
22	21	G	L	E	E	A	<u>Q</u>	F	W	L	22
23	40	A	V	L	G	N	<u>L</u>	T	I	I	22
24	206	I	S	A	I	G	<u>L</u>	D	S	L	22
25	11	A	T	Y	F	I	<u>L</u>	I	G	L	21
26	60	P	M	Y	I	F	<u>L</u>	C	M	L	21
27	135	A	T	V	L	T	<u>L</u>	P	R	V	21

HLA-A*0201 nonomers (SEQ ID
NOS 1463-1569, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
28	160	P	L	P	V	F	I	K	Q	L	21
29	174	N	I	L	S	H	S	Y	C	L	21
30	207	S	A	I	G	L	D	S	L	L	21
31	272	P	L	P	V	I	L	A	N	I	21
32	283	L	V	P	P	V	L	N	P	I	21
33	67	M	L	S	G	I	D	I	L	I	20
34	101	L	Q	I	F	A	I	H	S	L	20
35	282	L	L	V	P	P	V	L	N	P	20
36	299	E	I	R	Q	R	I	L	R	L	20
37	304	I	L	R	L	F	H	V	A	T	20
38	39	I	A	V	L	G	N	L	T	I	19
39	45	L	T	I	I	Y	I	V	R	T	19
40	92	T	T	I	Q	F	D	A	C	L	19
41	110	S	G	M	E	S	T	V	L	L	19
42	127	A	I	C	H	P	L	R	H	A	19
43	132	L	R	H	A	T	V	L	T	L	19
44	149	A	A	V	V	R	G	A	A	L	19
45	155	A	A	L	M	A	P	L	P	V	19
46	156	A	L	M	A	P	L	P	V	F	19
47	203	I	V	I	I	S	A	I	G	L	19
48	208	A	I	G	L	D	S	L	L	I	19
49	216	I	S	F	S	Y	L	L	I	L	19
50	219	S	Y	L	L	I	L	K	T	V	19
51	221	L	L	I	L	K	T	V	L	G	19
52	223	I	L	K	T	V	L	G	L	T	19
53	17	I	G	L	P	G	L	E	E	A	18
54	33	L	C	S	L	Y	L	I	A	V	18
55	34	C	S	L	Y	L	I	A	V	L	18
56	38	L	I	A	V	L	G	N	L	T	18
57	43	G	N	L	T	I	I	Y	I	V	18
58	85	A	I	F	W	F	N	S	T	T	18
59	118	L	A	M	A	F	D	R	Y	V	18
60	194	I	R	V	N	V	V	Y	G	L	18
61	210	G	L	D	S	L	L	I	S	F	18
62	215	L	I	S	F	S	Y	L	L	I	18
63	246	V	C	A	V	F	I	F	Y	V	18
64	254	V	P	F	I	G	L	S	M	V	18
65	15	I	L	I	G	L	P	G	L	E	17
66	63	I	F	L	C	M	L	S	G	I	17
67	72	D	I	L	I	S	T	S	S	M	17
68	93	T	I	Q	F	D	A	C	L	L	17
69	98	A	C	L	L	Q	I	F	A	I	17
70	111	G	M	E	S	T	V	L	L	A	17
71	120	M	A	F	D	R	Y	V	A	I	17
72	167	Q	L	P	F	C	R	S	N	I	17
73	197	N	V	V	Y	G	L	I	V	I	17
74	226	T	V	L	G	L	T	R	E	A	17
75	281	Y	L	L	V	P	P	V	L	N	17
76	31	F	P	L	C	S	L	Y	L	I	16

HLA-A*0201 nonomers (SEQ ID
NOS 1463-1569, respectively
in order of appearance)

Pos		1	2	3	4	5	6	7	8	9	score
77	56	S	L	H	E	P	<u>M</u>	Y	I	F	16
78	70	G	I	D	I	L	<u>I</u>	S	T	S	16
79	78	S	S	M	P	K	<u>M</u>	L	A	I	16
80	79	S	M	P	K	M	<u>L</u>	A	I	F	16
81	104	F	A	I	H	S	<u>L</u>	S	G	M	16
82	119	A	M	A	F	D	<u>R</u>	Y	V	A	16
83	144	T	K	I	G	V	<u>A</u>	A	V	V	16
84	147	G	V	A	A	V	<u>V</u>	R	G	A	16
85	186	V	M	K	L	A	<u>C</u>	D	D	I	16
86	230	L	T	R	E	A	<u>Q</u>	A	K	A	16
87	238	A	F	G	T	C	<u>V</u>	S	H	V	16
88	249	V	F	I	F	Y	<u>V</u>	P	F	I	16
89	302	Q	R	I	L	R	<u>L</u>	F	H	V	16
90	303	R	I	L	R	L	<u>F</u>	H	V	A	16
91	18	G	L	P	G	L	<u>E</u>	E	A	Q	15
92	35	S	L	Y	L	I	<u>A</u>	V	L	G	15
93	42	L	G	N	L	T	<u>I</u>	I	Y	I	15
94	46	T	I	I	Y	I	<u>V</u>	R	T	E	15
95	69	S	G	I	D	I	<u>L</u>	I	S	T	15
96	76	S	T	S	S	M	<u>P</u>	K	M	L	15
97	131	P	L	R	H	A	<u>T</u>	V	L	T	15
98	137	V	L	T	L	P	<u>R</u>	V	T	K	15
99	153	R	G	A	A	L	<u>M</u>	A	P	L	15
100	190	A	C	D	D	I	<u>R</u>	V	N	V	15
101	191	C	D	D	I	R	<u>V</u>	N	V	V	15
102	204	V	I	I	S	A	<u>I</u>	G	L	D	15
103	241	T	C	V	S	H	<u>V</u>	C	A	V	15
104	251	I	F	Y	V	P	<u>F</u>	I	G	L	15
105	269	R	D	S	P	L	<u>P</u>	V	I	L	15
106	280	I	Y	L	L	V	<u>P</u>	P	V	L	15
107	306	R	L	F	H	V	A	T	H	A	15

HLA A*0203 nonomers (SEQ ID
NOS 1570-1594, respectively
in order of appearance)

Pos		1	2	3	4	5	6	7	8	9	score
1	148	V	<u>A</u>	A	V	V	R	<u>G</u>	A	A	14
2	119	A	<u>M</u>	A	F	D	R	<u>Y</u>	V	A	13
3	147	G	<u>V</u>	A	A	V	V	<u>R</u>	G	A	12
4	97	D	<u>A</u>	C	L	L	Q	<u>I</u>	F	A	11
5	127	A	<u>I</u>	C	H	P	L	<u>R</u>	H	A	10
6	3	D	<u>P</u>	N	G	N	E	<u>S</u>	S	A	9
7	17	I	<u>G</u>	L	P	G	L	<u>E</u>	E	A	9
8	22	L	<u>E</u>	E	A	Q	F	<u>W</u>	L	A	9
9	32	P	<u>L</u>	C	S	L	Y	<u>L</u>	I	A	9
10	77	T	<u>S</u>	S	M	P	K	<u>M</u>	L	A	9
11	90	N	<u>S</u>	T	T	I	Q	<u>F</u>	D	A	9
12	111	G	M	E	S	T	V	L	L	A	9

HLA A*0203 nonomers (SEQ ID
NOS 1570-1594, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
13	113	E	S	T	V	L	L	A	M	A	9
14	141	P	R	V	T	K	I	G	V	A	9
15	142	R	V	T	K	I	G	V	A	A	9
16	151	V	V	R	G	A	A	L	M	A	9
17	182	L	H	Q	D	V	M	K	L	A	9
18	200	Y	G	L	I	V	I	I	S	A	9
19	226	T	V	L	G	L	T	R	E	A	9
20	228	L	G	L	T	R	E	A	Q	A	9
21	230	L	T	R	E	A	Q	A	K	A	9
22	240	G	T	C	V	S	H	V	C	A	9
23	270	D	S	P	L	P	V	I	L	A	9
24	303	R	I	L	R	L	F	H	V	A	9
25	306	R	L	F	H	V	A	T	H	A	9

HLA-A26 nonomers (SEQ ID NOS
1595-1675, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	299	E	I	R	Q	R	I	L	R	L	30
2	72	D	I	L	I	S	T	S	S	M	27
3	248	A	V	F	I	F	Y	V	P	F	27
4	210	G	L	D	S	L	L	I	S	F	26
5	14	F	I	L	I	G	L	P	G	L	24
6	56	S	L	H	E	P	M	Y	I	F	24
7	117	L	L	A	M	A	F	D	R	Y	24
8	222	L	I	L	K	T	V	L	G	L	24
9	245	H	V	C	A	V	F	I	F	Y	24
10	11	A	T	Y	F	I	L	I	G	L	23
11	37	Y	L	I	A	V	L	G	N	L	23
12	114	S	T	V	L	L	A	M	A	F	23
13	156	A	L	M	A	P	L	P	V	F	23
14	162	P	V	F	I	K	Q	L	P	F	23
15	181	C	L	H	Q	D	V	M	K	L	23
16	28	W	L	A	F	P	L	C	S	L	22
17	92	T	T	I	Q	F	D	A	C	L	22
18	160	P	L	P	V	F	I	K	Q	L	22
19	203	I	V	I	I	S	A	I	G	L	22
20	213	S	L	L	I	S	F	S	Y	L	22
21	275	V	I	L	A	N	I	Y	L	L	22
22	193	D	I	R	V	N	V	V	Y	G	21
23	242	C	V	S	H	V	C	A	V	F	21
24	76	S	T	S	S	M	P	K	M	L	20
25	253	Y	V	P	F	I	G	L	S	M	20
26	274	P	V	I	L	A	N	I	Y	L	20
27	23	E	E	A	Q	F	W	L	A	F	19
28	41	V	L	G	N	L	T	I	I	Y	19
29	49	Y	I	V	R	T	E	H	S	L	19
30	150	A	V	V	R	G	A	A	L	M	19

HLA-A26 nonomers (SEQ ID NOS
1595-1675, respectively in
order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
31	174	N I L S H S Y C L	19
32	192	D D I R V N V V Y	19
33	214	L L I S F S Y L L	19
34	251	I F Y V P F I G L	19
35	8	E S S A T Y F I L	18
36	21	G L E E A Q F W L	18
37	45	L T I I Y I V R T	18
38	54	E H S L H E P M Y	18
39	59	E P M Y I F L C M	18
40	88	W F N S T T I Q F	18
41	93	T I Q F D A C L L	18
42	185	D V M K L A C D D	18
43	198	V V Y G L I V I I	18
44	62	Y I F L C M L S G	17
45	70	G I D I L I S T S	17
46	79	S M P K M L A I F	17
47	96	F D A C L L Q I F	17
48	104	F A I H S L S G M	17
49	138	L T L P R V T K I	17
50	143	V T K I G V A A V	17
51	204	V I I S A I G L D	17
52	212	D S L L I S F S Y	17
53	220	Y L L I L K T V L	17
54	256	F I G L S M V H R	17
55	283	L V P P V L N P I	17
56	29	L A F P L C S L Y	16
57	40	A V L G N L T I I	16
58	46	T I I Y I V R T E	16
59	52	R T E H S L H E P	16
60	75	I S T S S M P K M	16
61	91	S T T I Q F D A C	16
62	135	A T V L T L P R V	16
63	147	G V A A V V R G A	16
64	201	G L I V I I S A I	16
65	257	I G L S M V H R F	16
66	279	N I Y L L V P P V	16
67	30	A F P L C S L Y L	15
68	101	L Q I F A I H S L	15
69	115	T V L L A M A F D	15
70	127	A I C H P L R H A	15
71	153	R G A A L M A P L	15
72	163	V F I K Q L P F C	15
73	215	L I S F S Y L L I	15
74	216	I S F S Y L L I L	15
75	225	K T V L G L T R E	15
76	272	P L P V I L A N I	15
77	282	L L V P P V L N P	15
78	286	P V L N P I V Y G	15
79	287	V L N P I V Y G V	15

HLA-A26 nonomers (SEQ ID NOS
1595-1675, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
80	296	K	T	K	E	I	R	Q	R	I	15
81	303	R	I	L	R	L	F	H	V	A	15

HLA-A3 nonomers (SEQ ID NOS
1676-1747, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	137	V	L	T	L	P	R	V	T	K	30
2	229	G	L	T	R	E	A	Q	A	K	27
3	145	K	I	G	V	A	A	V	V	R	26
4	150	A	V	V	R	G	A	A	L	M	24
5	290	P	I	V	Y	G	V	K	T	K	24
6	35	S	L	Y	L	I	A	V	L	G	23
7	156	A	L	M	A	P	L	P	V	F	23
8	47	I	I	Y	I	V	R	T	E	H	22
9	50	I	V	R	T	E	H	S	L	H	22
10	142	R	V	T	K	I	G	V	A	A	22
11	151	V	V	R	G	A	A	L	M	A	22
12	242	C	V	S	H	V	C	A	V	F	22
13	248	A	V	F	I	F	Y	V	P	F	22
14	116	V	L	L	A	M	A	F	D	R	21
15	192	D	D	I	R	V	N	V	V	Y	21
16	303	R	I	L	R	L	F	H	V	A	21
17	304	I	L	R	L	F	H	V	A	T	21
18	108	S	L	S	G	M	E	S	T	V	20
19	198	V	V	Y	G	L	I	V	I	I	20
20	291	I	V	Y	G	V	K	T	K	E	20
21	15	I	L	I	G	L	P	G	L	E	19
22	44	N	L	T	I	I	Y	I	V	R	19
23	73	I	L	I	S	T	S	S	M	P	19
24	74	L	I	S	T	S	S	M	P	K	19
25	99	C	L	L	Q	I	F	A	I	H	19
26	162	P	V	F	I	K	Q	L	P	F	19
27	203	I	V	I	I	S	A	I	G	L	19
28	221	L	L	I	L	K	T	V	L	G	19
29	245	H	V	C	A	V	F	I	F	Y	19
30	306	R	L	F	H	V	A	T	H	A	19
31	40	A	V	L	G	N	L	T	I	I	18
32	85	A	I	F	W	F	N	S	T	T	18
33	205	I	I	S	A	I	G	L	D	S	18
34	220	Y	L	L	I	L	K	T	V	L	18
35	253	Y	V	P	F	I	G	L	S	M	18
36	37	Y	L	I	A	V	L	G	N	L	17
37	41	V	L	G	N	L	T	I	I	Y	17
38	117	L	L	A	M	A	F	D	R	Y	17
39	131	P	L	R	H	A	T	V	L	T	17
40	136	T	V	L	T	L	P	R	V	T	17
41	180	Y	C	L	H	Q	D	V	M	K	17

HLA-A3 nonomers (SEQ ID NOS
1676-1747, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
42	201	G	L	I	V	I	I	S	A	I	17
43	213	S	L	L	I	S	F	S	Y	L	17
44	256	F	I	G	L	S	M	V	H	R	17
45	261	M	V	H	R	F	S	K	R	R	17
46	276	I	L	A	N	I	Y	L	L	V	17
47	281	Y	L	L	V	P	P	V	L	N	17
48	286	P	V	L	N	P	I	V	Y	G	17
49	288	L	N	P	I	V	Y	G	V	K	17
50	309	H	V	A	T	H	A	S	E	P	17
51	1	M	V	D	P	N	G	N	E	S	16
52	56	S	L	H	E	P	M	Y	I	F	16
53	70	G	I	D	I	L	I	S	T	S	16
54	72	D	I	L	I	S	T	S	S	M	16
55	115	T	V	L	L	A	M	A	F	D	16
56	125	Y	V	A	I	C	H	P	L	R	16
57	144	T	K	I	G	V	A	A	V	V	16
58	167	Q	L	P	F	C	R	S	N	I	16
59	175	I	L	S	H	S	Y	C	L	H	16
60	195	R	V	N	V	V	Y	G	L	I	16
61	197	N	V	V	Y	G	L	I	V	I	16
62	210	G	L	D	S	L	L	I	S	F	16
63	282	L	L	V	P	P	V	L	N	P	16
64	299	E	I	R	Q	R	I	L	R	L	16
65	301	R	Q	R	I	L	R	L	F	H	16
66	16	L	I	G	L	P	G	L	E	E	15
67	46	T	I	I	Y	I	V	R	T	E	15
68	102	Q	I	F	A	I	H	S	L	S	15
69	193	D	I	R	V	N	V	V	Y	G	15
70	208	A	I	G	L	D	S	L	L	I	15
71	223	I	L	K	T	V	L	G	L	T	15
72	237	K	A	F	G	T	C	V	S	H	15

HLA-B*0702 nonomers (SEQ ID
NOS 1748-1812, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	130	H	P	L	R	H	A	T	V	L	22
2	59	E	P	M	Y	I	F	L	C	M	21
3	168	L	P	F	C	R	S	N	I	L	20
4	289	N	P	I	V	Y	G	V	K	T	19
5	3	D	P	N	G	N	E	S	S	A	18
6	19	L	P	G	L	E	E	A	Q	F	18
7	140	L	P	R	V	T	K	I	G	V	18
8	284	V	P	P	V	L	N	P	I	V	17
9	31	F	P	L	C	S	L	Y	L	I	16
10	254	V	P	F	I	G	L	S	M	V	16
11	269	R	D	S	P	L	P	V	I	L	16
12	149	A	A	V	V	R	G	A	A	L	15

HLA-B*0702 nonomers (SEQ ID
 NOS 1748-1812, respectively
 in order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
13	153	R G A A L M A P L	15
14	156	A L M A P L P V F	15
15	251	I F Y V P F I G L	15
16	299	E I R Q R I L R L	15
17	8	E S S A T Y F I L	14
18	28	W L A F P L C S L	14
19	30	A F P L C S L Y L	14
20	110	S G M E S T V L L	14
21	132	L R H A T V L T L	14
22	159	A P L P V F I K Q	14
23	222	L I L K T V L G L	14
24	271	S P L P V I L A N	14
25	25	A Q F W L A F P L	13
26	109	L S G M E S T V L	13
27	124	R Y V A I C H P L	13
28	216	I S F S Y L L I L	13
29	268	R R D S P L P V I	13
30	280	I Y L L V P P V L	13
31	11	A T Y F I L I G L	12
32	34	C S L Y L I A V L	12
33	57	L H E P M Y I F L	12
34	76	S T S S M P K M L	12
35	142	R V T K I G V A A	12
36	151	V V R G A A L M A	12
37	190	A C D D I R V N V	12
38	194	I R V N V V Y G L	12
39	206	I S A I G L D S L	12
40	207	S A I G L D S L L	12
41	220	Y L L I L K T V L	12
42	267	K R R D S P L P V	12
43	304	I L R L F H V A T	12
44	14	F I L I G L P G L	11
45	23	E E A Q F W L A F	11
46	37	Y L I A V L G N L	11
47	40	A V L G N L T I I	11
48	77	T S S M P K M L A	11
49	78	S S M P K M L A I	11
50	80	M P K M L A I F W	11
51	92	T T I Q F D A C L	11
52	112	M E S T V L L A M	11
53	119	A M A F D R Y V A	11
54	127	A I C H P L R H A	11
55	131	P L R H A T V L T	11
56	155	A A L M A P L P V	11
57	157	L M A P L P V F I	11
58	181	C L H Q D V M K L	11
59	203	I V I I S A I G L	11
60	208	A I G L D S L L I	11
61	213	S L L I S F S Y L	11

HLA-B*0702 nonomers (SEQ ID
NOS 1748-1812, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
62	248	A	V	F	I	F	Y	V	P	F	11
63	265	F	S	K	R	R	D	S	P	L	11
64	275	V	I	L	A	N	I	Y	L	L	11
65	285	P	P	V	L	N	P	I	V	Y	11

HLA-B*08 nonomers (SEQ ID
NOS 1813-1847, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	299	E	I	R	Q	R	I	L	R	L	31
2	265	F	S	K	R	R	D	S	P	L	29
3	149	A	A	V	V	R	G	A	A	L	24
4	168	L	P	F	C	R	S	N	I	L	24
5	294	G	V	K	T	K	E	I	R	Q	21
6	120	M	A	F	D	R	Y	V	A	I	20
7	292	V	Y	G	V	K	T	K	E	I	20
8	21	G	L	E	E	A	Q	F	W	L	19
9	78	S	S	M	P	K	M	L	A	I	19
10	160	P	L	P	V	F	I	K	Q	L	19
11	186	V	M	K	L	A	C	D	D	I	18
12	213	S	L	L	I	S	F	S	Y	L	18
13	221	L	L	I	L	K	T	V	L	G	18
14	296	K	T	K	E	I	R	Q	R	I	18
15	297	T	K	E	I	R	Q	R	I	L	18
16	130	H	P	L	R	H	A	T	V	L	17
17	181	C	L	H	Q	D	V	M	K	L	17
18	223	I	L	K	T	V	L	G	L	T	17
19	28	W	L	A	F	P	L	C	S	L	16
20	37	Y	L	I	A	V	L	G	N	L	16
21	56	S	L	H	E	P	M	Y	I	F	16
22	80	M	P	K	M	L	A	I	F	W	16
23	162	P	V	F	I	K	Q	L	P	F	16
24	201	G	L	I	V	I	I	S	A	I	16
25	207	S	A	I	G	L	D	S	L	L	16
26	214	L	L	I	S	F	S	Y	L	L	16
27	220	Y	L	L	I	L	K	T	V	L	16
28	233	E	A	Q	A	K	A	F	G	T	16
29	275	V	I	L	A	N	I	Y	L	L	16
30	304	I	L	R	L	F	H	V	A	T	16
31	14	F	I	L	I	G	L	P	G	L	15
32	110	S	G	M	E	S	T	V	L	L	15
33	138	L	T	L	P	R	V	T	K	I	15
34	164	F	I	K	Q	L	P	F	C	R	15
35	222	L	I	L	K	T	V	L	G	L	15

HLA-B*1510 nonomers (SEQ ID
NOS 1848-1890, respectively
in order of appearance)

Pos		1	2	3	4	5	6	7	8	9	score
1	57	L	H	E	P	M	Y	I	F	L	23
2	244	S	H	V	C	A	V	F	I	F	17
3	269	R	D	S	P	L	P	V	I	L	16
4	280	I	Y	L	L	V	P	P	V	L	16
5	262	V	H	R	F	S	K	R	R	D	15
6	299	E	I	R	Q	R	I	L	R	L	15
7	106	I	H	S	L	S	G	M	E	S	14
8	206	I	S	A	I	G	L	D	S	L	14
9	220	Y	L	L	I	L	K	T	V	L	14
10	251	I	F	Y	V	P	F	I	G	L	14
11	297	T	K	E	I	R	Q	R	I	L	14
12	21	G	L	E	E	A	Q	F	W	L	13
13	34	C	S	L	Y	L	I	A	V	L	13
14	54	E	H	S	L	H	E	P	M	Y	13
15	110	S	G	M	E	S	T	V	L	L	13
16	194	I	R	V	N	V	V	Y	G	L	13
17	8	E	S	S	A	T	Y	F	I	L	12
18	14	F	I	L	I	G	L	P	G	L	12
19	28	W	L	A	F	P	L	C	S	L	12
20	66	C	M	L	S	G	I	D	I	L	12
21	76	S	T	S	S	M	P	K	M	L	12
22	92	T	T	I	Q	F	D	A	C	L	12
23	109	L	S	G	M	E	S	T	V	L	12
24	130	H	P	L	R	H	A	T	V	L	12
25	132	L	R	H	A	T	V	L	T	L	12
26	149	A	A	V	V	R	G	A	A	L	12
27	153	R	G	A	A	L	M	A	P	L	12
28	160	P	L	P	V	F	I	K	Q	L	12
29	181	C	L	H	Q	D	V	M	K	L	12
30	182	L	H	Q	D	V	M	K	L	A	12
31	203	I	V	I	I	S	A	I	G	L	12
32	216	I	S	F	S	Y	L	L	I	L	12
33	222	L	I	L	K	T	V	L	G	L	12
34	275	V	I	L	A	N	I	Y	L	L	12
35	37	Y	L	I	A	V	L	G	N	L	11
36	49	Y	I	V	R	T	E	H	S	L	11
37	93	T	I	Q	F	D	A	C	L	L	11
38	101	L	Q	I	F	A	I	H	S	L	11
39	129	C	H	P	L	R	H	A	T	V	11
40	133	R	H	A	T	V	L	T	L	P	11
41	177	S	H	S	Y	C	L	H	Q	D	11
42	207	S	A	I	G	L	D	S	L	L	11
43	257	I	G	L	S	M	V	H	R	F	11

HLA-B*2705 nonomers (SEQ ID
NOS 1891-2008, respectively
in order of appearance)

	Pos		1	2	3	4	5	6	7	8	9	score
1	194	I	R	V	N	V	V	Y	G	L		25
2	268	R	R	D	S	P	L	P	V	I		24
3	132	L	R	H	A	T	V	L	T	L		23

HLA-B*2705 nonomers (SEQ ID
NOS 1891-2008, respectively
in order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
4	300	I R Q R I L R L F	23
5	305	L R L F H V A T H	23
6	231	T R E A Q A K A F	21
7	34	C S L Y L I A V L	18
8	299	E I R Q R I L R L	18
9	6	G N E S S A T Y F	17
10	66	C M L S G I D I L	17
11	162	P V F I K Q L P F	17
12	207	S A I G L D S L L	17
13	210	G L D S L L I S F	17
14	220	Y L L I L K T V L	17
15	237	K A F G T C V S H	17
16	269	R D S P L P V I L	17
17	280	I Y L L V P P V L	17
18	295	V K T K E I R Q R	17
19	11	A T Y F I L I G L	16
20	14	F I L I G L P G L	16
21	21	G L E E A Q F W L	16
22	25	A Q F W L A F P L	16
23	37	Y L I A V L G N L	16
24	92	T T I Q F D A C L	16
25	101	L Q I F A I H S L	16
26	124	R Y V A I C H P L	16
27	130	H P L R H A T V L	16
28	141	P R V T K I G V A	16
29	153	R G A A L M A P L	16
30	181	C L H Q D V M K L	16
31	201	G L I V I I S A I	16
32	203	I V I I S A I G L	16
33	216	I S F S Y L L I L	16
34	222	L I L K T V L G L	16
35	255	P F I G L S M V H	16
36	257	I G L S M V H R F	16
37	275	V I L A N I Y L L	16
38	47	I I Y I V R T E H	15
39	109	L S G M E S T V L	15
40	114	S T V L L A M A F	15
41	123	D R Y V A I C H P	15
42	145	K I G V A A V V R	15
43	156	A L M A P L P V F	15
44	168	L P F C R S N I L	15
45	172	R S N I L S H S Y	15
46	198	V V Y G L I V I I	15
47	206	I S A I G L D S L	15
48	229	G L T R E A Q A K	15
49	248	A V F I F Y V P F	15
50	251	I F Y V P F I G L	15
51	274	P V I L A N I Y L	15
52	290	P I V Y G V K T K	15

HLA-B*2705 nonomers (SEQ ID
NOS 1891-2008, respectively
in order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
53	298	K E I R Q R I L R	15
54	19	L P G L E E A Q F	14
55	29	L A F P L C S L Y	14
56	30	A F P L C S L Y L	14
57	39	I A V L G N L T I	14
58	40	A V L G N L T I I	14
59	79	S M P K M L A I F	14
60	81	P K M L A I F W F	14
61	99	C L L Q I F A I H	14
62	137	V L T L P R V T K	14
63	138	L T L P R V T K I	14
64	150	A V V R G A A L M	14
65	160	P L P V F I K Q L	14
66	174	N I L S H S Y C L	14
67	180	Y C L H Q D V M K	14
68	192	D D I R V N V V Y	14
69	212	D S L L I S F S Y	14
70	213	S L L I S F S Y L	14
71	214	L L I S F S Y L L	14
72	260	S M V H R F S K R	14
73	263	H R F S K R R D S	14
74	267	K R R D S P L P V	14
75	293	Y G V K T K E I R	14
76	301	R Q R I L R L F H	14
77	302	Q R I L R L F H V	14
78	5	N G N E S S A T Y	13
79	23	E E A Q F W L A F	13
80	28	W L A F P L C S L	13
81	44	N L T I I Y I V R	13
82	51	V R T E H S L H E	13
83	56	S L H E P M Y I F	13
84	60	P M Y I F L C M L	13
85	72	D I L I S T S S M	13
86	74	L I S T S S M P K	13
87	75	I S T S S M P K M	13
88	98	A C L L Q I F A I	13
89	104	F A I H S L S G M	13
90	110	S G M E S T V L L	13
91	116	V L L A M A F D R	13
92	126	V A I C H P L R H	13
93	149	A A V V R G A A L	13
94	158	M A P L P V F I K	13
95	164	F I K Q L P F C R	13
96	170	F C R S N I L S H	13
97	171	C R S N I L S H S	13
98	187	M K L A C D D I R	13
99	217	S F S Y L L I L K	13
100	224	L K T V L G L T R	13
101	242	C V S H V C A V F	13

HLA-B*2705 nonomers(SEQ ID
NOS 1891-2008, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
102	256	F	I	G	L	S	M	V	H	R	13
103	261	M	V	H	R	F	S	K	R	R	13
104	49	Y	I	V	R	T	E	H	S	L	12
105	57	L	H	E	P	M	Y	I	F	L	12
106	88	W	F	N	S	T	T	I	Q	F	12
107	96	F	D	A	C	L	L	Q	I	F	12
108	134	H	A	T	V	L	T	L	P	R	12
109	152	V	R	G	A	A	L	M	A	P	12
110	179	S	Y	C	L	H	Q	D	V	M	12
111	197	N	V	V	Y	G	L	I	V	I	12
112	244	S	H	V	C	A	V	F	I	F	12
113	265	F	S	K	R	R	D	S	P	L	12
114	273	L	P	V	I	L	A	N	I	Y	12
115	285	P	P	V	L	N	P	I	V	Y	12
116	288	L	N	P	I	V	Y	G	V	K	12
117	296	K	T	K	E	I	R	Q	R	I	12
118	297	T	K	E	I	R	Q	R	I	L	12

HLA-B*2709 nonomers(SEQ ID
NOS 2009-2063, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	194	I	R	V	N	V	V	Y	G	L	24
2	268	R	R	D	S	P	L	P	V	I	24
3	132	L	R	H	A	T	V	L	T	L	22
4	267	K	R	R	D	S	P	L	P	V	21
5	300	I	R	Q	R	I	L	R	L	F	20
6	231	T	R	E	A	Q	A	K	A	F	19
7	302	Q	R	I	L	R	L	F	H	V	19
8	124	R	Y	V	A	I	C	H	P	L	16
9	269	R	D	S	P	L	P	V	I	L	16
10	43	G	N	L	T	I	I	Y	I	V	15
11	216	I	S	F	S	Y	L	L	I	L	15
12	11	A	T	Y	F	I	L	I	G	L	14
13	25	A	Q	F	W	L	A	F	P	L	14
14	153	R	G	A	A	L	M	A	P	L	14
15	174	N	I	L	S	H	S	Y	C	L	14
16	222	L	I	L	K	T	V	L	G	L	14
17	257	I	G	L	S	M	V	H	R	F	14
18	280	I	Y	L	L	V	P	P	V	L	14
19	6	G	N	E	S	S	A	T	Y	F	13
20	14	F	I	L	I	G	L	P	G	L	13
21	21	G	L	E	E	A	Q	F	W	L	13
22	66	C	M	L	S	G	I	D	I	L	13
23	130	H	P	L	R	H	A	T	V	L	13
24	201	G	L	I	V	I	I	S	A	I	13
25	203	I	V	I	I	S	A	I	G	L	13

HLA-B*2709 nonomers (SEQ ID
NOS 2009-2063, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
26	214	L	L	I	S	F	S	Y	L	L	13
27	251	I	F	Y	V	P	F	I	G	L	13
28	263	H	R	F	S	K	R	R	D	S	13
29	275	V	I	L	A	N	I	Y	L	L	13
30	305	L	R	L	F	H	V	A	T	H	13
31	30	A	F	P	L	C	S	L	Y	L	12
32	34	C	S	L	Y	L	I	A	V	L	12
33	37	Y	L	I	A	V	L	G	N	L	12
34	51	V	R	T	E	H	S	L	H	E	12
35	60	P	M	Y	I	F	L	C	M	L	12
36	75	I	S	T	S	S	M	P	K	M	12
37	93	T	I	Q	F	D	A	C	L	L	12
38	123	D	R	Y	V	A	I	C	H	P	12
39	135	A	T	V	L	T	L	P	R	V	12
40	138	L	T	L	P	R	V	T	K	I	12
41	149	A	A	V	V	R	G	A	A	L	12
42	155	A	A	L	M	A	P	L	P	V	12
43	168	L	P	F	C	R	S	N	I	L	12
44	181	C	L	H	Q	D	V	M	K	L	12
45	188	K	L	A	C	D	D	I	R	V	12
46	190	A	C	D	D	I	R	V	N	V	12
47	195	R	V	N	V	V	Y	G	L	I	12
48	210	G	L	D	S	L	L	I	S	F	12
49	213	S	L	L	I	S	F	S	Y	L	12
50	220	Y	L	L	I	L	K	T	V	L	12
51	248	A	V	F	I	F	Y	V	P	F	12
52	279	N	I	Y	L	L	V	P	P	V	12
53	287	V	L	N	P	I	V	Y	G	V	12
54	296	K	T	K	E	I	R	Q	R	I	12
55	299	E	I	R	Q	R	I	L	R	L	12

HLA-B*5101 nonomers (SEQ ID
NOS 2064-2132, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	39	I	A	V	L	G	N	L	T	I	26
2	31	F	P	L	C	S	L	Y	L	I	25
3	120	M	A	F	D	R	Y	V	A	I	24
4	130	H	P	L	R	H	A	T	V	L	23
5	118	L	A	M	A	F	D	R	Y	V	22
6	140	L	P	R	V	T	K	I	G	V	22
7	155	A	A	L	M	A	P	L	P	V	22
8	42	L	G	N	L	T	I	I	Y	I	21
9	254	V	P	F	I	G	L	S	M	V	21
10	284	V	P	P	V	L	N	P	I	V	21
11	168	L	P	F	C	R	S	N	I	L	20
12	235	Q	A	K	A	F	G	T	C	V	20
13	138	L	T	L	P	R	V	T	K	I	19

HLA-B*5101 nonomers (SEQ ID
 NOS 2064-2132, respectively
 in order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
14	159	A P L P V F I K Q	18
15	189	L A C D D I R V N	18
16	198	V V Y G L I V I I	18
17	277	L A N I Y L L V P	18
18	207	S A I G L D S L L	17
19	283	L V P P V L N P I	17
20	63	I F L C M L S G I	16
21	86	I F W F N S T T I	16
22	110	S G M E S T V L L	16
23	144	T K I G V A A V V	16
24	149	A A V V R G A A L	16
25	197	N V V Y G L I V I	16
26	271	S P L P V I L A N	16
27	280	I Y L L V P P V L	16
28	3	D P N G N E S S A	15
29	40	A V L G N L T I I	15
30	97	D A C L L Q I F A	15
31	132	L R H A T V L T L	15
32	222	L I L K T V L G L	15
33	279	N I Y L L V P P V	15
34	285	P P V L N P I V Y	15
35	289	N P I V Y G V K T	15
36	9	S S A T Y F I L I	14
37	65	L C M L S G I D I	14
38	84	L A I F W F N S T	14
39	126	V A I C H P L R H	14
40	157	L M A P L P V F I	14
41	158	M A P L P V F I K	14
42	191	C D D I R V N V V	14
43	200	Y G L I V I I S A	14
44	209	I G L D S L L I S	14
45	215	L I S F S Y L L I	14
46	219	S Y L L I L K T V	14
47	220	Y L L I L K T V L	14
48	237	K A F G T C V S H	14
49	247	C A V F I F Y V P	14
50	249	V F I F Y V P F I	14
51	251	I F Y V P F I G L	14
52	257	I G L S M V H R F	14
53	268	R R D S P L P V I	14
54	273	L P V I L A N I Y	14
55	29	L A F P L C S L Y	13
56	33	L C S L Y L I A V	13
57	55	H S L H E P M Y I	13
58	67	M L S G I D I L I	13
59	80	M P K M L A I F W	13
60	95	Q F D A C L L Q I	13
61	98	A C L L Q I F A I	13
62	104	F A I H S L S G M	13

HLA-B*5101 nonomers (SEQ ID
NOS 2064-2132, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
63	146	I	G	V	A	A	V	V	R	G	13
64	148	V	A	A	V	V	R	G	A	A	13
65	153	R	G	A	A	L	M	A	P	L	13
66	233	E	A	Q	A	K	A	F	G	T	13
67	243	V	S	H	V	C	A	V	F	I	13
68	292	V	Y	G	V	K	T	K	E	I	13
69	296	K	T	K	E	I	R	Q	R	I	13

Table XXVII, beginning at page 201, line 1, has been amended as follows:

Table XXVII:
HLA Class I decamers

HLA-A1 decamers (SEQ ID NOS
2133-2153, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	191	C	D	D	I	R	V	N	V	V	Y	27
2	244	S	H	V	C	A	V	F	I	F	Y	24
3	40	A	V	L	G	N	L	T	I	I	Y	21
4	284	V	P	P	V	L	N	P	I	V	Y	21
5	116	V	L	L	A	M	A	F	D	R	Y	20
6	28	W	L	A	F	P	L	C	S	L	Y	18
7	297	T	K	E	I	R	Q	R	I	L	R	17
8	21	G	L	E	E	A	Q	F	W	L	A	16
9	22	L	E	E	A	Q	F	W	L	A	F	16
10	52	R	T	E	H	S	L	H	E	P	M	16
11	53	T	E	H	S	L	H	E	P	M	Y	16
12	57	L	H	E	P	M	Y	I	F	L	C	16
13	111	G	M	E	S	T	V	L	L	A	M	16
14	272	P	L	P	V	I	L	A	N	I	Y	16
15	1	M	V	D	P	N	G	N	E	S	S	15
16	4	P	N	G	N	E	S	S	A	T	Y	15
17	121	A	F	D	R	Y	V	A	I	C	H	15
18	171	C	R	S	N	I	L	S	H	S	Y	15
19	211	L	D	S	L	L	I	S	F	S	Y	15
20	8	E	S	S	A	T	Y	F	I	L	I	13
21	190	A	C	D	D	I	R	V	N	V	V	13

HLA-A*0201 decamers (SEQ ID
NOS 2154-2253, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	221	L	L	I	L	K	T	V	L	G	L	30
2	100	L	L	Q	I	F	A	I	H	S	L	29
3	282	L	L	V	P	P	V	L	N	P	I	27
4	205	I	I	S	A	I	G	L	D	S	L	26
5	213	S	L	L	I	S	F	S	Y	L	L	25

HLA-A*0201 decamers (SEQ ID
NOS 2154-2253, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
6	56	S	L	H	E	P	<u>M</u>	Y	I	F	L	24
7	62	Y	I	F	L	C	<u>M</u>	L	S	G	I	24
8	108	S	L	S	G	M	<u>E</u>	S	T	V	L	24
9	117	L	L	A	M	A	<u>F</u>	D	R	Y	V	24
10	131	P	L	R	H	A	<u>T</u>	V	L	T	L	24
11	137	V	L	T	L	P	<u>R</u>	V	T	K	I	24
12	215	L	I	S	F	S	<u>Y</u>	L	L	I	L	24
13	38	L	I	A	V	L	<u>G</u>	N	L	T	I	23
14	41	V	L	G	N	L	<u>T</u>	I	I	Y	I	23
15	156	A	L	M	A	P	<u>L</u>	P	V	F	I	23
16	193	D	I	R	V	N	<u>V</u>	V	Y	G	L	23
17	214	L	L	I	S	F	<u>S</u>	Y	L	L	I	23
18	32	P	L	C	S	L	<u>Y</u>	L	I	A	V	22
19	119	A	M	A	F	D	<u>R</u>	Y	V	A	I	22
20	237	K	A	F	G	T	<u>C</u>	V	S	H	V	22
21	275	V	I	L	A	N	<u>I</u>	Y	L	L	V	22
22	85	A	I	F	W	F	<u>N</u>	S	T	T	I	21
23	139	T	L	P	R	V	<u>T</u>	K	I	G	V	21
24	202	L	I	V	I	I	<u>S</u>	A	I	G	L	21
25	13	Y	F	I	L	I	<u>G</u>	L	P	G	L	20
26	16	L	I	G	L	P	<u>G</u>	L	E	E	A	20
27	29	L	A	F	P	L	<u>C</u>	S	L	Y	L	20
28	142	R	V	T	K	I	<u>G</u>	V	A	A	V	20
29	148	V	A	A	V	V	<u>R</u>	G	A	A	L	20
30	167	Q	L	P	F	C	<u>R</u>	S	N	I	L	20
31	180	Y	C	L	H	Q	<u>D</u>	V	M	K	L	20
32	222	L	I	L	K	T	<u>V</u>	L	G	L	T	20
33	240	G	T	C	V	S	<u>H</u>	V	C	A	V	20
34	248	A	V	F	I	F	<u>Y</u>	V	P	F	I	20
35	250	F	I	F	Y	V	<u>P</u>	F	I	G	L	20
36	271	S	P	L	P	V	<u>I</u>	L	A	N	I	20
37	279	N	I	Y	L	L	<u>V</u>	P	P	V	L	20
38	304	I	L	R	L	F	<u>H</u>	V	A	T	H	20
39	10	S	A	T	Y	F	<u>I</u>	L	I	G	L	19
40	15	I	L	I	G	L	<u>P</u>	G	L	E	E	19
41	27	F	W	L	A	F	<u>P</u>	L	C	S	L	19
42	35	S	L	Y	L	I	<u>A</u>	V	L	G	N	19
43	37	Y	L	I	A	V	<u>L</u>	G	N	L	T	19
44	44	N	L	T	I	I	<u>Y</u>	I	V	R	T	19
45	64	F	L	C	M	L	<u>S</u>	G	I	D	I	19
46	83	M	L	A	I	F	<u>W</u>	F	N	S	T	19
47	159	A	P	L	P	V	<u>F</u>	I	K	Q	L	19
48	189	L	A	C	D	D	<u>I</u>	R	V	N	V	19
49	207	S	A	I	G	L	<u>D</u>	S	L	L	I	19
50	253	Y	V	P	F	I	<u>G</u>	L	S	M	V	19
51	276	I	L	A	N	I	<u>Y</u>	L	L	V	P	19
52	281	Y	L	L	V	P	<u>P</u>	V	L	N	P	19
53	283	L	V	P	P	V	<u>L</u>	N	P	I	V	19
54	286	P	V	L	N	P	<u>I</u>	V	Y	G	V	19
55	33	L	C	S	L	Y	<u>L</u>	I	A	V	L	18

HLA-A*0201 decamers (SEQ ID
NOS 2154-2253, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
56	36	L	Y	L	I	A	<u>V</u>	L	G	N	L	18
57	39	I	A	<u>V</u>	L	G	<u>N</u>	L	T	I	I	18
58	42	L	G	N	L	T	<u>I</u>	I	Y	I	V	18
59	66	C	M	L	S	G	<u>I</u>	D	I	L	I	18
60	111	G	M	E	S	T	<u>V</u>	L	L	A	M	18
61	128	I	C	H	P	L	<u>R</u>	H	A	T	V	18
62	134	H	A	T	<u>V</u>	L	T	L	P	R	V	18
63	154	G	A	A	L	M	<u>A</u>	P	L	P	V	18
64	157	L	M	A	P	L	<u>P</u>	V	F	I	K	18
65	190	A	C	D	D	I	<u>R</u>	V	N	V	V	18
66	229	G	L	T	R	E	<u>A</u>	Q	A	K	A	18
67	245	H	V	C	A	V	<u>F</u>	I	F	Y	V	18
68	274	P	V	I	L	A	<u>N</u>	I	Y	L	L	18
69	278	A	N	I	Y	L	<u>L</u>	V	P	P	V	18
70	291	I	V	Y	G	V	<u>K</u>	T	K	E	I	18
71	298	K	E	I	R	Q	<u>R</u>	I	L	R	L	18
72	48	I	Y	I	V	R	T	E	H	S	L	17
73	65	L	C	M	L	S	G	I	D	I	L	17
74	67	M	L	S	G	I	<u>D</u>	I	L	I	S	17
75	74	L	I	S	T	S	<u>S</u>	M	P	K	M	17
76	91	S	T	T	I	Q	<u>F</u>	D	A	C	L	17
77	94	I	Q	F	D	A	<u>C</u>	L	L	Q	I	17
78	188	K	L	A	C	D	<u>D</u>	I	R	V	N	17
79	197	N	V	V	Y	G	<u>L</u>	I	V	I	I	17
80	200	Y	G	L	I	V	<u>I</u>	I	S	A	I	17
81	218	F	S	Y	L	L	<u>I</u>	L	K	T	V	17
82	227	V	L	G	L	T	R	E	A	Q	A	17
83	303	R	I	L	R	L	<u>F</u>	H	V	A	T	17
84	21	G	L	E	E	A	<u>Q</u>	F	W	L	A	16
85	92	T	T	I	Q	<u>F</u>	D	A	C	L	L	16
86	97	D	A	C	L	L	<u>Q</u>	I	F	A	I	16
87	127	A	I	C	H	P	<u>L</u>	R	H	A	T	16
88	143	V	T	K	I	G	<u>V</u>	A	A	V	V	16
89	195	R	V	N	V	V	<u>Y</u>	G	L	I	V	16
90	220	Y	L	L	I	L	<u>K</u>	T	V	L	G	16
91	296	K	T	K	E	I	<u>R</u>	Q	R	I	L	16
92	18	G	L	P	G	L	E	E	A	Q	F	15
93	30	A	F	P	L	C	<u>S</u>	L	Y	L	I	15
94	126	V	A	I	C	H	P	L	R	H	A	15
95	145	K	I	G	V	A	<u>A</u>	V	V	R	G	15
96	173	S	N	I	L	S	<u>H</u>	S	Y	C	L	15
97	201	G	L	I	V	I	<u>I</u>	S	A	I	G	15
98	208	A	I	G	L	D	<u>S</u>	L	L	I	S	15
99	210	G	L	D	S	L	<u>L</u>	I	S	F	S	15
100	267	K	R	R	D	S	P	L	P	V	I	15

HLA-A*0203 decamers (SEQ ID
NOS 2254-2301, respectively
in order of appearance)

Pos 1 2 3 4 5 6 7 8 9 0 score

78

HLA-A*0203 decamers (SEQ ID
NOS 2254-2301, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	141	P	R	V	T	K	I	G	V	A	A	19
2	147	G	V	A	A	V	V	R	G	A	A	19
3	112	M	E	S	T	V	L	L	A	M	A	18
4	227	V	L	G	L	T	R	E	A	Q	A	18
5	229	G	L	T	R	E	A	Q	A	K	A	18
6	142	R	V	T	K	I	G	V	A	A	V	17
7	148	V	A	A	V	V	R	G	A	A	L	17
8	2	V	D	P	N	G	N	E	S	S	A	10
9	16	L	I	G	L	P	G	L	E	E	A	10
10	21	G	L	E	E	A	Q	F	W	L	A	10
11	31	F	P	L	C	S	L	Y	L	I	A	10
12	76	S	T	S	S	M	P	K	M	L	A	10
13	89	F	N	S	T	T	I	Q	F	D	A	10
14	96	F	D	A	C	L	L	Q	I	F	A	10
15	110	S	G	M	E	S	T	V	L	L	A	10
16	118	L	A	M	A	F	D	R	Y	V	A	10
17	126	V	A	I	C	H	P	L	R	H	A	10
18	140	L	P	R	V	T	K	I	G	V	A	10
19	146	I	G	V	A	A	V	V	R	G	A	10
20	150	A	V	V	R	G	A	A	L	M	A	10
21	181	C	L	H	Q	D	V	M	K	L	A	10
22	199	V	Y	G	L	I	V	I	I	S	A	10
23	225	K	T	V	L	G	L	T	R	E	A	10
24	239	F	G	T	C	V	S	H	V	C	A	10
25	269	R	D	S	P	L	P	V	I	L	A	10
26	302	Q	R	I	L	R	L	F	H	V	A	10
27	305	L	R	L	F	H	V	A	T	H	A	10
28	3	D	P	N	G	N	E	S	S	A	T	9
29	17	I	G	L	P	G	L	E	E	A	Q	9
30	22	L	E	E	A	Q	F	W	L	A	F	9
31	32	P	L	C	S	L	Y	L	I	A	V	9
32	77	T	S	S	M	P	K	M	L	A	I	9
33	90	N	S	T	T	I	Q	F	D	A	C	9
34	97	D	A	C	L	L	Q	I	F	A	I	9
35	111	G	M	E	S	T	V	L	L	A	M	9
36	113	E	S	T	V	L	L	A	M	A	F	9
37	119	A	M	A	F	D	R	Y	V	A	I	9
38	127	A	I	C	H	P	L	R	H	A	T	9
39	151	V	V	R	G	A	A	L	M	A	P	9
40	182	L	H	Q	D	V	M	K	L	A	C	9
41	200	Y	G	L	I	V	I	I	S	A	I	9
42	226	T	V	L	G	L	T	R	E	A	Q	9
43	228	L	G	L	T	R	E	A	Q	A	K	9
44	230	L	T	R	E	A	Q	A	K	A	F	9
45	240	G	T	C	V	S	H	V	C	A	V	9
46	270	D	S	P	L	P	V	I	L	A	N	9
47	303	R	I	L	R	L	F	H	V	A	T	9
48	306	R	L	F	H	V	A	T	H	A	S	9

HLA-A26 decamers(SEQ ID NOS
2302-2366, respectively in
order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	score
1 299	E	I	R	Q	R	I	L	R	L	F	31
2 193	D	I	R	V	N	V	V	Y	G	L	29
3 250	F	I	F	Y	V	P	F	I	G	L	25
4 256	F	I	G	L	S	M	V	H	R	F	25
5 74	L	I	S	T	S	S	M	P	K	M	24
6 274	P	V	I	L	A	N	I	Y	L	L	24
7 18	G	L	P	G	L	E	E	A	Q	F	23
8 116	V	L	L	A	M	A	F	D	R	Y	23
9 205	I	I	S	A	I	G	L	D	S	L	23
10 221	L	L	I	L	K	T	V	L	G	L	23
11 230	L	T	R	E	A	Q	A	K	A	F	23
12 13	Y	F	I	L	I	G	L	P	G	L	22
13 40	A	V	L	G	N	L	T	I	I	Y	22
14 56	S	L	H	E	P	M	Y	I	F	L	22
15 95	Q	F	D	A	C	L	L	Q	I	F	22
16 215	L	I	S	F	S	Y	L	L	I	L	22
17 92	T	T	I	Q	F	D	A	C	L	L	21
18 100	L	L	Q	I	F	A	I	H	S	L	21
19 103	I	F	A	I	H	S	L	S	G	M	21
20 296	K	T	K	E	I	R	Q	R	I	L	21
21 28	W	L	A	F	P	L	C	S	L	Y	20
22 131	P	L	R	H	A	T	V	L	T	L	20
23 59	E	P	M	Y	I	F	L	C	M	L	19
24 91	S	T	T	I	Q	F	D	A	C	L	19
25 202	L	I	V	I	I	S	A	I	G	L	19
26 212	D	S	L	L	I	S	F	S	Y	L	19
27 272	P	L	P	V	I	L	A	N	I	Y	19
28 279	N	I	Y	L	L	V	P	P	V	L	19
29 52	R	T	E	H	S	L	H	E	P	M	18
30 62	Y	I	F	L	C	M	L	S	G	I	18
31 72	D	I	L	I	S	T	S	S	M	P	18
32 108	S	L	S	G	M	E	S	T	V	L	18
33 113	E	S	T	V	L	L	A	M	A	F	18
34 151	V	V	R	G	A	A	L	M	A	P	18
35 78	S	S	M	P	K	M	L	A	I	F	17
36 142	R	V	T	K	I	G	V	A	A	V	17
37 162	P	V	F	I	K	Q	L	P	F	C	17
38 164	F	I	K	Q	L	P	F	C	R	S	17
39 167	Q	L	P	F	C	R	S	N	I	L	17
40 185	D	V	M	K	L	A	C	D	D	I	17
41 248	A	V	F	I	F	Y	V	P	F	I	17
42 253	Y	V	P	F	I	G	L	S	M	V	17
43 45	L	T	I	I	Y	I	V	R	T	E	16
44 145	K	I	G	V	A	A	V	V	R	G	16
45 198	V	V	Y	G	L	I	V	I	I	S	16
46 203	I	V	I	I	S	A	I	G	L	D	16
47 209	I	G	L	D	S	L	L	I	S	F	16
48 213	S	L	L	I	S	F	S	Y	L	L	16
49 255	P	F	I	G	L	S	M	V	H	R	16
50 264	R	F	S	K	R	R	D	S	P	L	16

HLA-A26 decamers (SEQ ID NOS
2302-2366, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
51	294	G	V	K	T	K	E	I	R	Q	R	16
52	16	L	I	G	L	P	G	L	E	E	A	15
53	80	M	P	K	M	L	A	I	F	W	F	15
54	114	S	T	V	L	L	A	M	A	F	D	15
55	155	A	A	L	M	A	P	L	P	V	F	15
56	159	A	P	L	P	V	F	I	K	Q	L	15
57	174	N	I	L	S	H	S	Y	C	L	H	15
58	197	N	V	V	Y	G	L	I	V	I	I	15
59	210	G	L	D	S	L	L	I	S	F	S	15
60	214	L	L	I	S	F	S	Y	L	L	I	15
61	222	L	I	L	K	T	V	L	G	L	T	15
62	240	G	T	C	V	S	H	V	C	A	V	15
63	247	C	A	V	F	I	F	Y	V	P	F	15
64	286	P	V	L	N	P	I	V	Y	G	V	15
65	298	K	E	I	R	Q	R	I	L	R	L	15

HLA-A3 decamers (SEQ ID NOS
2367-2432, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	136	T	V	<u>L</u>	T	L	<u>P</u>	R	V	T	K	31
2	287	V	L	<u>N</u>	P	I	<u>V</u>	Y	G	V	K	28
3	223	I	L	<u>K</u>	T	V	<u>L</u>	G	L	T	R	27
4	304	I	L	<u>R</u>	L	F	<u>H</u>	V	A	T	H	27
5	73	I	L	<u>I</u>	S	T	<u>S</u>	S	M	P	K	26
6	15	I	L	<u>I</u>	G	L	<u>P</u>	G	L	E	E	23
7	40	A	V	<u>L</u>	G	N	<u>L</u>	T	I	I	Y	23
8	150	A	V	<u>V</u>	R	G	<u>A</u>	A	L	M	A	23
9	258	G	L	<u>S</u>	M	V	<u>H</u>	R	F	S	K	23
10	18	G	L	<u>P</u>	G	L	<u>E</u>	E	A	Q	F	22
11	303	R	I	<u>L</u>	R	L	<u>F</u>	H	V	A	T	22
12	276	I	L	<u>A</u>	N	I	<u>Y</u>	L	L	V	P	21
13	28	W	L	<u>A</u>	F	P	<u>L</u>	C	S	L	Y	20
14	115	T	V	<u>L</u>	L	A	M	A	F	D	R	20
15	116	V	L	<u>L</u>	A	M	A	F	D	R	Y	20
16	125	Y	V	<u>A</u>	I	C	<u>H</u>	P	L	R	H	20
17	131	P	L	<u>R</u>	H	A	T	V	L	T	L	20
18	144	T	K	<u>I</u>	G	V	<u>A</u>	A	V	V	R	20
19	156	A	L	M	A	P	<u>L</u>	P	V	F	I	20
20	195	R	V	<u>N</u>	V	V	<u>Y</u>	G	L	I	V	20
21	35	S	L	<u>Y</u>	L	I	<u>A</u>	V	L	G	N	19
22	272	P	L	<u>P</u>	V	I	<u>L</u>	A	N	I	Y	19
23	37	Y	L	<u>I</u>	A	V	<u>L</u>	G	N	L	T	18
24	49	Y	I	<u>V</u>	R	T	<u>E</u>	H	S	L	H	18
25	50	I	V	<u>R</u>	T	<u>E</u>	H	S	L	H	E	18
26	108	S	L	<u>S</u>	G	M	<u>E</u>	S	T	V	L	18
27	142	R	V	<u>T</u>	K	I	<u>G</u>	V	A	A	V	18
28	188	K	L	<u>A</u>	C	D	<u>D</u>	I	R	V	N	18
29	279	N	I	<u>Y</u>	L	L	<u>V</u>	P	P	V	L	18
30	291	I	V	<u>Y</u>	G	V	<u>K</u>	T	K	E	I	18

HLA-A3 decamers (SEQ ID NOS
2367-2432, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
31	294	G	V	K	T	K	E	I	R	Q	R	18
32	46	T	I	I	Y	I	V	R	T	E	H	17
33	102	Q	I	F	A	I	H	S	L	S	G	17
34	151	V	V	R	G	A	A	L	M	A	P	17
35	179	S	Y	C	L	H	Q	D	V	M	K	17
36	203	I	V	I	I	S	A	I	G	L	D	17
37	204	V	I	I	S	A	I	G	L	D	S	17
38	220	Y	L	L	I	L	K	T	V	L	G	17
39	221	L	L	I	L	K	T	V	L	G	L	17
40	227	V	L	G	L	T	R	E	A	Q	A	17
41	242	C	V	S	H	V	C	A	V	F	I	17
42	289	N	P	I	V	Y	G	V	K	T	K	17
43	38	L	I	A	V	L	G	N	L	T	I	16
44	85	A	I	F	W	F	N	S	T	T	I	16
45	147	G	V	A	A	V	V	R	G	A	A	16
46	198	V	V	Y	G	L	I	V	I	I	S	16
47	201	G	L	I	V	I	I	S	A	I	G	16
48	214	L	L	I	S	F	S	Y	L	L	I	16
49	226	T	V	L	G	L	T	R	E	A	Q	16
50	228	L	G	L	T	R	E	A	Q	A	K	16
51	229	G	L	T	R	E	A	Q	A	K	A	16
52	1	M	V	D	P	N	G	N	E	S	S	15
53	44	N	L	T	I	I	Y	I	V	R	T	15
54	47	I	I	Y	I	V	R	T	E	H	S	15
55	67	M	L	S	G	I	D	I	L	I	S	15
56	72	D	I	L	I	S	T	S	S	M	P	15
57	99	C	L	L	Q	I	F	A	I	H	S	15
58	105	A	I	H	S	L	S	G	M	E	S	15
59	145	K	I	G	V	A	A	V	V	R	G	15
60	175	I	L	S	H	S	Y	C	L	H	Q	15
61	191	C	D	D	I	R	V	N	V	V	Y	15
62	208	A	I	G	L	D	S	L	L	I	S	15
63	275	V	I	L	A	N	I	Y	L	L	V	15
64	281	Y	L	L	V	P	P	V	L	N	P	15
65	299	E	I	R	Q	R	I	L	R	L	F	15
66	306	R	L	F	H	V	A	T	H	A	S	15

HLA-B*0702 decamers (SEQ ID
NOS 2433-2492, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	159	A	P	L	P	V	F	I	K	Q	L	23
2	59	E	P	M	Y	I	F	L	C	M	L	22
3	273	L	P	V	I	L	A	N	I	Y	L	20
4	3	D	P	N	G	N	E	S	S	A	T	19
5	130	H	P	L	R	H	A	T	V	L	T	19
6	140	L	P	R	V	T	K	I	G	V	A	19
7	161	L	P	V	F	I	K	Q	L	P	F	19
8	31	F	P	L	C	S	L	Y	L	I	A	18
9	271	S	P	L	P	V	I	L	A	N	I	18

HLA-B*0702 decamers (SEQ ID
NOS 2433-2492, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
10	80	M	P	K	M	L	A	I	F	W	F	16
11	108	S	L	S	G	M	E	S	T	V	L	16
12	131	P	L	R	H	A	T	V	L	T	L	15
13	264	R	F	S	K	R	R	D	S	P	L	15
14	33	L	C	S	L	Y	L	I	A	V	L	14
15	109	L	S	G	M	E	S	T	V	L	L	14
16	152	V	R	G	A	A	L	M	A	P	L	14
17	205	I	I	S	A	I	G	L	D	S	L	14
18	215	L	I	S	F	S	Y	L	L	I	L	14
19	268	R	R	D	S	P	L	P	V	I	L	14
20	29	L	A	F	P	L	C	S	L	Y	L	13
21	148	V	A	A	V	V	R	G	A	A	L	13
22	156	A	L	M	A	P	L	P	V	F	I	13
23	193	D	I	R	V	N	V	V	Y	G	L	13
24	221	L	L	I	L	K	T	V	L	G	L	13
25	298	K	E	I	R	Q	R	I	L	R	L	13
26	7	N	E	S	S	A	T	Y	F	I	L	12
27	19	L	P	G	L	E	E	A	Q	F	W	12
28	24	E	A	Q	F	W	L	A	F	P	L	12
29	119	A	M	A	F	D	R	Y	V	A	I	12
30	129	C	H	P	L	R	H	A	T	V	L	12
31	206	I	S	A	I	G	L	D	S	L	L	12
32	219	S	Y	L	L	I	L	K	T	V	L	12
33	279	N	I	Y	L	L	V	P	P	V	L	12
34	285	P	P	V	L	N	P	I	V	Y	G	12
35	8	E	S	S	A	T	Y	F	I	L	I	11
36	13	Y	F	I	L	I	G	L	P	G	L	11
37	27	F	W	L	A	F	P	L	C	S	L	11
38	48	I	Y	I	V	R	T	E	H	S	L	11
39	56	S	L	H	E	P	M	Y	I	F	L	11
40	65	L	C	M	L	S	G	I	D	I	L	11
41	75	I	S	T	S	S	M	P	K	M	L	11
42	77	T	S	S	M	P	K	M	L	A	I	11
43	91	S	T	T	I	Q	F	D	A	C	L	11
44	123	D	R	Y	V	A	I	C	H	P	L	11
45	142	R	V	T	K	I	G	V	A	A	V	11
46	180	Y	C	L	H	Q	D	V	M	K	L	11
47	190	A	C	D	D	I	R	V	N	V	V	11
48	212	D	S	L	L	I	S	F	S	Y	L	11
49	234	A	Q	A	K	A	F	G	T	C	V	11
50	242	C	V	S	H	V	C	A	V	F	I	11
51	248	A	V	F	I	F	Y	V	P	F	I	11
52	250	F	I	F	Y	V	P	F	I	G	L	11
53	254	V	P	F	I	G	L	S	M	V	H	11
54	266	S	K	R	R	D	S	P	L	P	V	11
55	267	K	R	R	D	S	P	L	P	V	I	11
56	269	R	D	S	P	L	P	V	I	L	A	11
57	278	A	N	I	Y	L	L	V	P	P	V	11
58	284	V	P	P	V	L	N	P	I	V	Y	11
59	289	N	P	I	V	Y	G	V	K	T	K	11

HLA-B*0702 decamers (SEQ ID
NOS 2433-2492, respectively
in order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	score
60 296	K	T	K	E	I	R	Q	R	I	L	11

Table XXVIII, beginning at page 205, line 1, has been amended as follows:

Table XXVIII:

HLA Class II Epitopes (sample 15-mer length)

(SEQ ID NOS 2493-2595, respectively in order of appearance)

HLA-DRB1*0101 15-mers

Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
1 200	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	L	36
2 68	L	S	G	I	D	I	L	I	S	T	S	S	M	P	K	34
3 62	Y	I	F	L	C	M	L	S	G	I	D	I	L	I	S	33
4 103	I	F	A	I	H	S	L	S	G	M	E	S	T	V	L	32
5 45	L	T	I	I	Y	I	V	R	T	E	H	S	L	H	E	31
6 193	D	I	R	V	N	V	V	Y	G	L	I	V	I	I	S	31
7 277	L	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	31
8 97	D	A	C	L	L	Q	I	F	A	I	H	S	L	S	G	30
9 106	I	H	S	L	S	G	M	E	S	T	V	L	L	A	M	30
10 240	G	T	C	V	S	H	V	C	A	V	F	I	F	Y	V	30
11 10	S	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	29
12 289	N	P	I	V	Y	G	V	K	T	K	E	I	R	Q	R	29
13 11	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	A	28
14 250	F	I	F	Y	V	P	F	I	G	L	S	M	V	H	R	27
15 140	L	P	R	V	T	K	I	G	V	A	A	V	V	R	G	26
16 183	H	Q	D	V	M	K	L	A	C	D	D	I	R	V	N	26
17 217	S	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	26
18 16	L	I	G	L	P	G	L	E	E	A	Q	F	W	L	A	25
19 24	E	A	Q	F	W	L	A	F	P	L	C	S	L	Y	L	25
20 36	L	Y	L	I	A	V	L	G	N	L	T	I	I	Y	I	25
21 70	G	I	D	I	L	I	S	T	S	S	M	P	K	M	L	25
22 111	G	M	E	S	T	V	L	L	A	M	A	F	D	R	Y	25
23 148	V	A	A	V	V	R	G	A	A	L	M	A	P	L	P	25
24 162	P	V	F	I	K	Q	L	P	F	C	R	S	N	I	L	25
25 197	N	V	V	Y	G	L	I	V	I	I	S	A	I	G	L	25
26 211	L	D	S	L	L	I	S	F	S	Y	L	L	I	L	K	25
27 218	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	R	25
28 13	Y	F	I	L	I	G	L	P	G	L	E	E	A	Q	F	24
29 30	A	F	P	L	C	S	L	Y	L	I	A	V	L	G	N	24
30 39	I	A	V	L	G	N	L	T	I	I	Y	I	V	R	T	24
31 77	T	S	S	M	P	K	M	L	A	I	F	W	F	N	S	24
32 85	A	I	F	W	F	N	S	T	T	I	Q	F	D	A	C	24
33 137	V	L	T	L	P	R	V	T	K	I	G	V	A	A	V	24
34 151	V	V	R	G	A	A	L	M	A	P	L	P	V	F	I	24
35 161	L	P	V	F	I	K	Q	L	P	F	C	R	S	N	I	24
36 196	V	N	V	V	Y	G	L	I	V	I	I	S	A	I	G	24

HLA-DRB1*0101 15-mers

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
37	202	L	I	V	I	I	S	A	I	G	L	D	S	L	L	I	24
38	208	A	I	G	L	D	S	L	L	I	S	F	S	Y	L	L	24
39	248	A	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	24
40	251	I	F	Y	V	P	F	I	G	L	S	M	V	H	R	F	24
41	83	M	L	A	I	F	W	F	N	S	T	T	I	Q	F	D	23
42	101	L	Q	I	F	A	I	H	S	L	S	G	M	E	S	T	23
43	165	I	K	Q	L	P	F	C	R	S	N	I	L	S	H	S	23
44	203	I	V	I	I	S	A	I	G	L	D	S	L	L	I	S	23
45	221	L	L	I	L	K	T	V	L	G	L	T	R	E	A	Q	23
46	278	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	V	23
47	27	F	W	L	A	F	P	L	C	S	L	Y	L	I	A	V	22
48	35	S	L	Y	L	I	A	V	L	G	N	L	T	I	I	Y	22
49	61	M	Y	I	F	L	C	M	L	S	G	I	D	I	L	I	22
50	65	L	C	M	L	S	G	I	D	I	L	I	S	T	S	S	22
51	80	M	P	K	M	L	A	I	F	W	F	N	S	T	T	I	22
52	145	K	I	G	V	A	A	V	V	R	G	A	A	L	M	A	22
53	146	I	G	V	A	A	V	V	R	G	A	A	L	M	A	P	22
54	154	G	A	A	L	M	A	P	L	P	V	F	I	K	Q	L	22
55	205	I	I	S	A	I	G	L	D	S	L	L	I	S	F	S	22
56	243	V	S	H	V	C	A	V	F	I	F	Y	V	P	F	I	22
57	270	D	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	22
58	274	P	V	I	L	A	N	I	Y	L	L	V	P	P	V	L	22
59	281	Y	L	L	V	P	P	V	L	N	P	I	V	Y	G	V	22
60	34	C	S	L	Y	L	I	A	V	L	G	N	L	T	I	I	21
61	69	S	G	I	D	I	L	I	S	T	S	S	M	P	K	M	21
62	152	V	R	G	A	A	L	M	A	P	L	P	V	F	I	K	21
63	299	E	I	R	Q	R	I	L	R	L	F	H	V	A	T	H	21
64	100	L	L	Q	I	F	A	I	H	S	L	S	G	M	E	S	20
65	135	A	T	V	L	T	L	P	R	V	T	K	I	G	V	A	20
66	141	P	R	V	T	K	I	G	V	A	A	V	V	R	G	A	20
67	191	C	D	D	I	R	V	N	V	V	Y	G	L	I	V	I	20
68	199	V	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	20
69	262	V	H	R	F	S	K	R	R	D	S	P	L	P	V	I	20
70	271	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	P	20
71	28	W	L	A	F	P	L	C	S	L	Y	L	I	A	V	L	19
72	58	H	E	P	M	Y	I	F	L	C	M	L	S	G	I	D	19
73	59	E	P	M	Y	I	F	L	C	M	L	S	G	I	D	I	19
74	60	P	M	Y	I	F	L	C	M	L	S	G	I	D	I	L	19
75	98	A	C	L	L	Q	I	F	A	I	H	S	L	S	G	M	19
76	215	L	I	S	F	S	Y	L	L	I	L	K	T	V	L	G	19
77	219	S	Y	L	L	I	L	K	T	V	L	G	L	T	R	E	19
78	228	L	G	L	T	R	E	A	Q	A	K	A	F	G	T	C	19
79	232	R	E	A	Q	A	K	A	F	G	T	C	V	S	H	V	19
80	246	V	C	A	V	F	I	F	Y	V	P	F	I	G	L	S	19
81	297	T	K	E	I	R	Q	R	I	L	R	L	F	H	V	A	19
82	3	D	P	N	G	N	E	S	S	A	T	Y	F	I	L	I	18
83	14	F	I	L	I	G	L	P	G	L	E	E	A	Q	F	W	18
84	25	A	Q	F	W	L	A	F	P	L	C	S	L	Y	L	I	18
85	42	L	G	N	L	T	I	I	Y	I	V	R	T	E	H	S	18
86	46	T	I	I	Y	I	V	R	T	E	H	S	L	H	E	P	18
87	78	S	S	M	P	K	M	L	A	I	F	W	F	N	S	T	18

HLA-DRB1*0101 15-mers

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
88	84	L	A	I	F	W	F	N	S	T	T	I	Q	F	D	A	18
89	89	F	N	S	T	T	I	Q	F	D	A	C	L	L	Q	I	18
90	93	T	I	Q	F	D	A	C	L	L	Q	I	F	A	I	H	18
91	115	T	V	L	L	A	M	A	F	D	R	Y	V	A	I	C	18
92	119	A	M	A	F	D	R	Y	V	A	I	C	H	P	L	R	18
93	127	A	I	C	H	P	L	R	H	A	T	V	L	T	L	P	18
94	129	C	H	P	L	R	H	A	T	V	L	T	L	P	R	V	18
95	147	G	V	A	A	V	V	R	G	A	A	L	M	A	P	L	18
96	149	A	A	V	V	R	G	A	A	L	M	A	P	L	P	V	18
97	216	I	S	F	S	Y	L	L	I	L	K	T	V	L	G	L	18
98	227	V	L	G	L	T	R	E	A	Q	A	K	A	F	G	T	18
99	249	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	H	18
100	253	Y	V	P	F	I	G	L	S	M	V	H	R	F	S	K	18
101	284	V	P	P	V	L	N	P	I	V	Y	G	V	K	T	K	18
102	286	P	V	L	N	P	I	V	Y	G	V	K	T	K	E	I	18
103	303	R	I	L	R	L	F	H	V	A	T	H	A	S	E	P	18

HLA-DRB1*0301 (DR17) 15-mers
 (SEQ ID NOS 2596-2671, respectively
 in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
1	16	L	I	G	L	P	G	L	E	E	A	Q	F	W	L	A	26
2	206	I	S	A	I	G	L	D	S	L	L	I	S	F	S	Y	23
3	91	S	T	T	I	Q	F	D	A	C	L	L	Q	I	F	A	22
4	117	L	L	A	M	A	F	D	R	Y	V	A	I	C	H	P	22
5	38	L	I	A	V	L	G	N	L	T	I	I	Y	I	V	R	21
6	179	S	Y	C	L	H	Q	D	V	M	K	L	A	C	D	D	21
7	211	L	D	S	L	L	I	S	F	S	Y	L	L	I	L	K	21
8	219	S	Y	L	L	I	L	K	T	V	L	G	L	T	R	E	21
9	272	P	L	P	V	I	L	A	N	I	Y	L	L	V	P	P	21
10	26	Q	F	W	L	A	F	P	L	C	S	L	Y	L	I	A	20
11	114	S	T	V	L	L	A	M	A	F	D	R	Y	V	A	I	20
12	129	C	H	P	L	R	H	A	T	V	L	T	L	P	R	V	20
13	134	H	A	T	V	L	T	L	P	R	V	T	K	I	G	V	20
14	186	V	M	K	L	A	C	D	D	I	R	V	N	V	V	Y	20
15	200	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	L	20
16	270	D	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	20
17	297	T	K	E	I	R	Q	R	I	L	R	L	F	H	V	A	20
18	11	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	A	19
19	54	E	H	S	L	H	E	P	M	Y	I	F	L	C	M	L	19
20	106	I	H	S	L	S	G	M	E	S	T	V	L	L	A	M	19
21	165	I	K	Q	L	P	F	C	R	S	N	I	L	S	H	S	19
22	191	C	D	D	I	R	V	N	V	Y	G	L	I	V	I		19
23	203	I	V	I	I	S	A	I	G	L	D	S	L	L	I	S	19
24	213	S	L	L	I	S	F	S	Y	L	L	I	L	K	T	V	19
25	224	L	K	T	V	L	G	L	T	R	E	A	Q	A	K	A	19
26	227	V	L	G	L	T	R	E	A	Q	A	K	A	F	G	T	19
27	248	A	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	19
28	254	V	P	F	I	G	L	S	M	V	H	R	F	S	K	R	19
29	277	L	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	19

HLA-DRB1*0301 (DR17) 15-mers
(SEQ ID NOS 2596-2671, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
30	36	L	Y	L	I	A	V	L	G	N	L	T	I	I	Y	I	18
31	93	T	I	Q	F	D	A	C	L	L	Q	I	F	A	I	H	18
32	98	A	C	L	L	Q	I	F	A	I	H	S	L	S	G	M	18
33	125	Y	V	A	I	C	H	P	L	R	H	A	T	V	L	T	18
34	158	M	A	P	L	P	V	F	I	K	Q	L	P	F	C	R	18
35	187	M	K	L	A	C	D	D	I	R	V	N	V	V	Y	G	18
36	217	S	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	18
37	225	K	T	V	L	G	L	T	R	E	A	Q	A	K	A	F	18
38	281	Y	L	L	V	P	P	V	L	N	P	I	V	Y	G	V	18
39	288	L	N	P	I	V	Y	G	V	K	T	K	E	I	R	Q	18
40	18	G	L	P	G	L	E	E	A	Q	F	W	L	A	F	P	17
41	44	N	L	T	I	I	Y	I	V	R	T	E	H	S	L	H	17
42	145	K	I	G	V	A	A	V	V	R	G	A	A	L	M	A	17
43	159	A	P	L	P	V	F	I	K	Q	L	P	F	C	R	S	17
44	256	F	I	G	L	S	M	V	H	R	F	S	K	R	R	D	17
45	259	L	S	M	V	H	R	F	S	K	R	R	D	S	P	L	17
46	137	V	L	T	L	P	R	V	T	K	I	G	V	A	A	V	16
47	262	V	H	R	F	S	K	R	R	D	S	P	L	P	V	I	16
48	294	G	V	K	T	K	E	I	R	Q	R	I	L	R	L	F	16
49	46	T	I	I	Y	I	V	R	T	E	H	S	L	H	E	P	15
50	51	V	R	T	E	H	S	L	H	E	P	M	Y	I	F	L	15
51	172	R	S	N	I	L	S	H	S	Y	C	L	H	Q	D	V	15
52	189	L	A	C	D	D	I	R	V	N	V	V	Y	G	L	I	15
53	212	D	S	L	L	I	S	F	S	Y	L	L	I	L	K	T	15
54	218	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	R	15
55	271	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	P	15
56	279	N	I	Y	L	L	V	P	P	V	L	N	P	I	V	Y	15
57	12	T	Y	F	I	L	I	G	L	P	G	L	E	E	A	Q	14
58	35	S	L	Y	L	I	A	V	L	G	N	L	T	I	I	Y	14
59	64	F	L	C	M	L	S	G	I	D	I	L	I	S	T	S	14
60	140	L	P	R	V	T	K	I	G	V	A	A	V	V	R	G	14
61	273	L	P	V	I	L	A	N	I	Y	L	L	V	P	P	V	14
62	301	R	Q	R	I	L	R	L	F	H	V	A	T	H	A	S	14
63	13	Y	F	I	L	I	G	L	P	G	L	E	E	A	Q	F	13
64	47	I	I	Y	I	V	R	T	E	H	S	L	H	E	P	M	13
65	71	I	D	I	L	I	S	T	S	S	M	P	K	M	L	A	13
66	80	M	P	K	M	L	A	I	F	W	F	N	S	T	T	I	13
67	109	L	S	G	M	E	S	T	V	L	L	A	M	A	F	D	13
68	113	E	S	T	V	L	L	A	M	A	F	D	R	Y	V	A	13
69	135	A	T	V	L	T	L	P	R	V	T	K	I	G	V	A	13
70	195	R	V	N	V	V	Y	G	L	I	V	I	I	S	A	I	13
71	202	L	I	V	I	I	S	A	I	G	L	D	S	L	L	I	13
72	220	Y	L	L	I	L	K	T	V	L	G	L	T	R	E	A	13
73	221	L	L	I	L	K	T	V	L	G	L	T	R	E	A	Q	13
74	264	R	F	S	K	R	R	D	S	P	L	P	V	I	L	A	13
75	280	I	Y	L	L	V	P	P	V	L	N	P	I	V	Y	G	13
76	302	Q	R	I	L	R	L	F	H	V	A	T	H	A	S	E	13

HLA-DRB1*0401 (DR4Dw4) 15-mers
 (SEQ ID NOS 2672-2805, respectively
 in order of appearance)

Pos		1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
1	36	L	Y	L	I	A	V	L	G	N	L	T	I	I	Y	I	26
2	45	L	T	I	I	Y	I	V	R	T	E	H	S	L	H	E	26
3	68	L	S	G	I	D	I	L	I	S	T	S	S	M	P	K	26
4	83	M	L	A	I	F	W	F	N	S	T	T	I	Q	F	D	26
5	134	H	A	T	V	L	T	L	P	R	V	T	K	I	G	V	26
6	145	K	I	G	V	A	A	V	V	R	G	A	A	L	M	A	26
7	224	L	K	T	V	L	G	L	T	R	E	A	Q	A	K	A	26
8	227	V	L	G	L	T	R	E	A	Q	A	K	A	F	G	T	26
9	256	F	I	G	L	S	M	V	H	R	F	S	K	R	R	D	26
10	281	Y	L	L	V	P	P	V	L	N	P	I	V	Y	G	V	26
11	289	N	P	I	V	Y	G	V	K	T	K	E	I	R	Q	R	26
12	301	R	Q	R	I	L	R	L	F	H	V	A	T	H	A	S	26
13	11	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	A	22
14	24	E	A	Q	F	W	L	A	F	P	L	C	S	L	Y	L	22
15	25	A	Q	F	W	L	A	F	P	L	C	S	L	Y	L	I	22
16	34	C	S	L	Y	L	I	A	V	L	G	N	L	T	I	I	22
17	84	L	A	I	F	W	F	N	S	T	T	I	Q	F	D	A	22
18	122	F	D	R	Y	V	A	I	C	H	P	L	R	H	A	T	22
19	197	N	V	V	Y	G	L	I	V	I	I	S	A	I	G	L	22
20	215	L	I	S	F	S	Y	L	L	I	L	K	T	V	L	G	22
21	217	S	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	22
22	250	F	I	F	Y	V	P	F	I	G	L	S	M	V	H	R	22
23	278	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	V	22
24	19	L	P	G	L	E	E	A	Q	F	W	L	A	F	P	L	20
25	30	A	F	P	L	C	S	L	Y	L	I	A	V	L	G	N	20
26	33	L	C	S	L	Y	L	I	A	V	L	G	N	L	T	I	20
27	35	S	L	Y	L	I	A	V	L	G	N	L	T	I	I	Y	20
28	39	I	A	V	L	G	N	L	T	I	I	Y	I	V	R	T	20
29	42	L	G	N	L	T	I	I	Y	I	V	R	T	E	H	S	20
30	44	N	L	T	I	I	Y	I	V	R	T	E	H	S	L	H	20
31	48	I	Y	I	V	R	T	E	H	S	L	H	E	P	M	Y	20
32	58	H	E	P	M	Y	I	F	L	C	M	L	S	G	I	D	20
33	62	Y	I	F	L	C	M	L	S	G	I	D	I	L	I	S	20
34	65	L	C	M	L	S	G	I	D	I	L	I	S	T	S	S	20
35	71	I	D	I	L	I	S	T	S	S	M	P	K	M	L	A	20
36	80	M	P	K	M	L	A	I	F	W	F	N	S	T	T	I	20
37	81	P	K	M	L	A	I	F	W	F	N	S	T	T	I	Q	20
38	91	S	T	T	I	Q	F	D	A	C	L	L	Q	I	F	A	20
39	97	D	A	C	L	L	Q	I	F	A	I	H	S	L	S	G	20
40	98	A	C	L	L	Q	I	F	A	I	H	S	L	S	G	M	20
41	100	L	L	Q	I	F	A	I	H	S	L	S	G	M	E	S	20
42	103	I	F	A	I	H	S	L	S	G	M	E	S	T	V	L	20
43	106	I	H	S	L	S	G	M	E	S	T	V	L	L	A	M	20
44	115	T	V	L	L	A	M	A	F	D	R	Y	V	A	I	C	20
45	117	L	L	A	M	A	F	D	R	Y	V	A	I	C	H	P	20
46	125	Y	V	A	I	C	H	P	L	R	H	A	T	V	L	T	20
47	129	C	H	P	L	R	H	A	T	V	L	T	L	P	R	V	20
48	137	V	L	T	L	P	R	V	T	K	I	G	V	A	A	V	20
49	140	L	P	R	V	T	K	I	G	V	A	A	V	V	R	G	20

HLA-DRB1*0401 (DR4Dw4) 15-mers
(SEQ ID NOS 2672-2805, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
50	155	A	A	L	M	A	P	L	P	V	F	I	K	Q	L	P	20
51	162	P	V	F	I	K	Q	L	P	F	C	R	S	N	I	L	20
52	165	I	K	Q	L	P	F	C	R	S	N	I	L	S	H	S	20
53	179	S	Y	C	L	H	Q	D	V	M	K	L	A	C	D	D	20
54	183	H	Q	D	V	M	K	L	A	C	D	D	I	R	V	N	20
55	186	V	M	K	L	A	C	D	D	I	R	V	N	V	V	Y	20
56	193	D	I	R	V	N	V	V	Y	G	L	I	V	I	I	S	20
57	196	V	N	V	V	Y	G	L	I	V	I	I	S	A	I	G	20
58	199	V	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	20
59	200	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	L	20
60	202	L	I	V	I	I	S	A	I	G	L	D	S	L	L	I	20
61	203	I	V	I	I	S	A	I	G	L	D	S	L	L	I	S	20
62	206	I	S	A	I	G	L	D	S	L	L	I	S	F	S	Y	20
63	208	A	I	G	L	D	S	L	L	I	S	F	S	Y	L	L	20
64	211	L	D	S	L	L	I	S	F	S	Y	L	L	I	L	K	20
65	212	D	S	L	L	I	S	F	S	Y	L	L	I	L	K	T	20
66	218	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	R	20
67	240	G	T	C	V	S	H	V	C	A	V	F	I	F	Y	V	20
68	243	V	S	H	V	C	A	V	F	I	F	Y	V	P	F	I	20
69	246	V	C	A	V	F	I	F	Y	V	P	F	I	G	L	S	20
70	248	A	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	20
71	251	I	F	Y	V	P	F	I	G	L	S	M	V	H	R	F	20
72	272	P	L	P	V	I	L	A	N	I	Y	L	L	V	P	P	20
73	277	L	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	20
74	285	P	P	V	L	N	P	I	V	Y	G	V	K	T	K	E	20
75	18	G	L	P	G	L	E	E	A	Q	F	W	L	A	F	P	18
76	27	F	W	L	A	F	P	L	C	S	L	Y	L	I	A	V	18
77	69	S	G	I	D	I	L	I	S	T	S	S	M	P	K	M	18
78	94	I	Q	F	D	A	C	L	L	Q	I	F	A	I	H	S	18
79	99	C	L	L	Q	I	F	A	I	H	S	L	S	G	M	E	18
80	107	H	S	L	S	G	M	E	S	T	V	L	L	A	M	A	18
81	116	V	L	L	A	M	A	F	D	R	Y	V	A	I	C	H	18
82	126	V	A	I	C	H	P	L	R	H	A	T	V	L	T	L	18
83	164	F	I	K	Q	L	P	F	C	R	S	N	I	L	S	H	18
84	176	L	S	H	S	Y	C	L	H	Q	D	V	M	K	L	A	18
85	187	M	K	L	A	C	D	D	I	R	V	N	V	V	Y	G	18
86	205	I	I	S	A	I	G	L	D	S	L	L	I	S	F	S	18
87	233	E	A	Q	A	K	A	F	G	T	C	V	S	H	V	C	18
88	237	K	A	F	G	T	C	V	S	H	V	C	A	V	F	I	18
89	271	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	P	18
90	293	Y	G	V	K	T	K	E	I	R	Q	R	I	L	R	L	18
91	294	G	V	K	T	K	E	I	R	Q	R	I	L	R	L	F	18
92	10	S	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	16
93	28	W	L	A	F	P	L	C	S	L	Y	L	I	A	V	L	16
94	59	E	P	M	Y	I	F	L	C	M	L	S	G	I	D	I	16
95	61	M	Y	I	F	L	C	M	L	S	G	I	D	I	L	I	16
96	85	A	I	F	W	F	N	S	T	T	I	Q	F	D	A	C	16
97	101	L	Q	I	F	A	I	H	S	L	S	G	M	E	S	T	16
98	177	S	H	S	Y	C	L	H	Q	D	V	M	K	L	A	C	16

HLA-DRB1*0401 (DR4Dw4) 15-mers
(SEQ ID NOS 2672-2805, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
99	236	A	K	A	F	G	T	C	V	S	H	V	C	A	V	F	16
100	249	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	H	16
101	253	Y	V	P	F	I	G	L	S	M	V	H	R	F	S	K	16
102	13	Y	F	I	L	I	G	L	P	G	L	E	E	A	Q	F	14
103	14	F	I	L	I	G	L	P	G	L	E	E	A	Q	F	W	14
104	16	L	I	G	L	P	G	L	E	E	A	Q	F	W	L	A	14
105	38	L	I	A	V	L	G	N	L	T	I	I	Y	I	V	R	14
106	47	I	I	Y	I	V	R	T	E	H	S	L	H	E	P	M	14
107	54	E	H	S	L	H	E	P	M	Y	I	F	L	C	M	L	14
108	60	P	M	Y	I	F	L	C	M	L	S	G	I	D	I	L	14
109	64	F	L	C	M	L	S	G	I	D	I	L	I	S	T	S	14
110	70	G	I	D	I	L	I	S	T	S	S	M	P	K	M	L	14
111	72	D	I	L	I	S	T	S	S	M	P	K	M	L	A	I	14
112	109	L	S	G	M	E	S	T	V	L	L	A	M	A	F	D	14
113	113	E	S	T	V	L	L	A	M	A	F	D	R	Y	V	A	14
114	135	A	T	V	L	T	L	P	R	V	T	K	I	G	V	A	14
115	143	V	T	K	I	G	V	A	A	V	V	R	G	A	A	L	14
116	148	V	A	A	V	V	R	G	A	A	L	M	A	P	L	P	14
117	149	A	A	V	V	R	G	A	A	L	M	A	P	L	P	V	14
118	154	G	A	A	L	M	A	P	L	P	V	F	I	K	Q	L	14
119	158	M	A	P	L	P	V	F	I	K	Q	L	P	F	C	R	14
120	173	S	N	I	L	S	H	S	Y	C	L	H	Q	D	V	M	14
121	184	Q	D	V	M	K	L	A	C	D	D	I	R	V	N	V	14
122	191	C	D	D	I	R	V	N	V	V	Y	G	L	I	V	I	14
123	195	R	V	N	V	V	Y	G	L	I	V	I	I	S	A	I	14
124	213	S	L	L	I	S	F	S	Y	L	L	I	L	K	T	V	14
125	220	Y	L	L	I	L	K	T	V	L	G	L	T	R	E	A	14
126	221	L	L	I	L	K	T	V	L	G	L	T	R	E	A	Q	14
127	225	K	T	V	L	G	L	T	R	E	A	Q	A	K	A	F	14
128	259	L	S	M	V	H	R	F	S	K	R	R	D	S	P	L	14
129	270	D	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	14
130	273	L	P	V	I	L	A	N	I	Y	L	L	V	P	P	V	14
131	274	P	V	I	L	A	N	I	Y	L	L	V	P	P	V	L	14
132	280	I	Y	L	L	V	P	P	V	L	N	P	I	V	Y	G	14
133	284	V	P	P	V	L	N	P	I	V	Y	G	V	K	T	K	14
134	302	Q	R	I	L	R	L	F	H	V	A	T	H	A	S	E	14

HLA-DRB1*1101 15-mers
(SEQ ID NOS 2806-2866, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
1	145	K	I	G	V	A	A	V	V	R	G	A	A	L	M	A	28
2	122	F	D	R	Y	V	A	I	C	H	P	L	R	H	A	T	25
3	217	S	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	25
4	197	N	V	V	Y	G	L	I	V	I	I	S	A	I	G	L	24
5	10	S	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	23
6	255	P	F	I	G	L	S	M	V	H	R	F	S	K	R	R	23
7	44	N	L	T	I	I	Y	I	V	R	T	E	H	S	L	H	22

HLA-DRB1*1101 15-mers

(SEQ ID NOS 2806-2866, respectively
in order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
8 59	E	P	M	Y	I	F	L	C	M	L	S	G	I	D	I	22
9 158	M	A	P	L	P	V	F	I	K	Q	L	P	F	C	R	22
10 237	K	A	F	G	T	C	V	S	H	V	C	A	V	F	I	22
11 74	L	I	S	T	S	S	M	P	K	M	L	A	I	F	W	21
12 134	H	A	T	V	L	T	L	P	R	V	T	K	I	G	V	20
13 137	V	L	T	L	P	R	V	T	K	I	G	V	A	A	V	20
14 162	P	V	F	I	K	Q	L	P	F	C	R	S	N	I	L	20
15 199	V	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	20
16 224	L	K	T	V	L	G	L	T	R	E	A	Q	A	K	A	20
17 256	F	I	G	L	S	M	V	H	R	F	S	K	R	R	D	20
18 290	P	I	V	Y	G	V	K	T	K	E	I	R	Q	R	I	20
19 301	R	Q	R	I	L	R	L	F	H	V	A	T	H	A	S	20
20 65	L	C	M	L	S	G	I	D	I	L	I	S	T	S	S	19
21 100	L	L	Q	I	F	A	I	H	S	L	S	G	M	E	S	19
22 196	V	N	V	V	Y	G	L	I	V	I	I	S	A	I	G	19
23 218	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	R	19
24 247	C	A	V	F	I	F	Y	V	P	F	I	G	L	S	M	19
25 274	P	V	I	L	A	N	I	Y	L	L	V	P	P	V	L	19
26 45	L	T	I	I	Y	I	V	R	T	E	H	S	L	H	E	18
27 68	L	S	G	I	D	I	L	I	S	T	S	S	M	P	K	18
28 80	M	P	K	M	L	A	I	F	W	F	N	S	T	T	I	18
29 97	D	A	C	L	L	Q	I	F	A	I	H	S	L	S	G	18
30 103	I	F	A	I	H	S	L	S	G	M	E	S	T	V	L	18
31 208	A	I	G	L	D	S	L	L	I	S	F	S	Y	L	L	18
32 249	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	H	18
33 61	M	Y	I	F	L	C	M	L	S	G	I	D	I	L	I	17
34 215	L	I	S	F	S	Y	L	L	I	L	K	T	V	L	G	17
35 259	L	S	M	V	H	R	F	S	K	R	R	D	S	P	L	17
36 278	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	V	17
37 288	L	N	P	I	V	Y	G	V	K	T	K	E	I	R	Q	17
38 11	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	A	16
39 24	E	A	Q	F	W	L	A	F	P	L	C	S	L	Y	L	16
40 42	L	G	N	L	T	I	I	Y	I	V	R	T	E	H	S	16
41 253	Y	V	P	F	I	G	L	S	M	V	H	R	F	S	K	16
42 47	I	I	Y	I	V	R	T	E	H	S	L	H	E	P	M	15
43 99	C	L	L	Q	I	F	A	I	H	S	L	S	G	M	E	15
44 116	V	L	L	A	M	A	F	D	R	Y	V	A	I	C	H	15
45 143	V	T	K	I	G	V	A	A	V	V	R	G	A	A	L	15
46 179	S	Y	C	L	H	Q	D	V	M	K	L	A	C	D	D	15
47 227	V	L	G	L	T	R	E	A	Q	A	K	A	F	G	T	15
48 260	S	M	V	H	R	F	S	K	R	R	D	S	P	L	P	15
49 261	M	V	H	R	F	S	K	R	R	D	S	P	L	P	V	15
50 277	L	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	15
51 285	P	P	V	L	N	P	I	V	Y	G	V	K	T	K	E	15
52 114	S	T	V	L	L	A	M	A	F	D	R	Y	V	A	I	14
53 125	Y	V	A	I	C	H	P	L	R	H	A	T	V	L	T	14
54 126	V	A	I	C	H	P	L	R	H	A	T	V	L	T	L	14
55 140	L	P	R	V	T	K	I	G	V	A	A	V	V	R	G	14
56 170	F	C	R	S	N	I	L	S	H	S	Y	C	L	H	Q	14

HLA-DRB1*1101 15-mers

(SEQ ID NOS 2806-2866, respectively
in order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
57 180	Y	C	L	H	Q	D	V	M	K	L	A	C	D	D	I	14
58 193	D	I	R	V	N	V	V	Y	G	L	I	V	I	I	S	14
59 229	G	L	T	R	E	A	Q	A	K	A	F	G	T	C	V	14
60 270	D	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	14
61 298	K	E	I	R	Q	R	I	L	R	L	F	H	V	A	T	14

Table XXIX, beginning at page 213, line 1, has been amended as follows:

Table XXIX. Nucleotide sequence in the 5' region close to 101P3A11 gene (SEQ ID NO: 2867).

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1  TCGGCTCCAC CAAGCCTGGC TAACTTTTGC ATTTTAAATA GAGGCAGGGT TTCACCATGT
61 TGGCCTGGCT GGTCTCGAAC CCCTGACCTT GCGATCTGCC CACCTCGGCC TCCCAAAGTG
121 CTGGGATTAC AGGCGTGAGC CACTGTACCT GGCGGGGCTT ATTGTTTTTT AAAAAGATTT
181 CCAAAACCTT GCCCTGGCAA TTCTGATTTT CTGGGCCTGG AGCAGGACCT GGAGGGATGG
241 TGTTGTCAAT TACTTTAGAT GTTTCTATCA GGAAAGTTTG AGAAATGGTA TTCAGGCCCTA
301 AACACAAACC TCTCTTGAAG TCTCATCCCA GACTGAGCCC CTGCTCCCTA TCTTAAATTA
361 GATTATAGTA GGTCTTAAAG TCAGCTGTAG ACTGAGCCTC TAAATCTGAA CCCAGACCCA
421 CCCTAACCCC AGGATACATC AGAAGAGCTG GTCAATGTGG ACCATTCTGA GCAATCCTGC
481 AAGTCTACTC TGATGGGAAA AGGCTAAGAG CAGTGCCCTG GGCAGCAACA TCAGCTCTGA
541 AGATGCAGGA CTGTGTTACA TGTTTTATGA GTGGGTCTTC ACACACTGAG ATTCATGGGA
601 CAGTAATAGA ATCTGCTTGT GCAGCACTGG GGCCTTGGAG GGTCAGGGTA AGGCTCAAGA
661 TGTCCAGGAA GTTGTATATA AGGAGAATCA GAGCAGAGAG AGACTAGGGT TCAGAATTAC
721 CAGGATGACT TAGTCCTGTT TGTTACTGTC ACCACTCCAA TGCCTTTTCC TCATTAGTCC
781 TTTCTCTCCT CTGAGCCACA ACTAAATGAT GTTTCTACTT TTCCCTTTCT ACTTTCCTAG
841 ACCCTGGATT TTGTATGCAG AAGCCCCAGC TCTTGGTCCC TATCATAGCC ACTTCAAATG
901 GAAATCTGGT CCACGCAGCA TACTTCCTTT TGGTGGGTAT CCCTGGCCTG GGGCCTACCA
961 TACACTTTTG GCTGGCTTTC CCACTGTGTT TTATGTATGC CTTGGCCACC CTGGGTAACC
1021 TGACCATTGT CCTCATCATT CGTGTGGAGA GGCAGCTGCA TGAGCCCATG TACCTCTTCC
1081 TGGCCATGCT TTCCACTATT GACCTAGTCC TCTCCTCTAT CACCATGCCC AAGATGGCCA
1141 GTCTTTTCTT GATGGGCATC CAGGAGATCG AGTTCAACAT TTGCCTGGCC CAGATGTTCC
1201 TTATCCATGC TCTGTCAGCC GTGGAGTCAG CTGTCCTGCT GGCCATGGCT TTTGACCGCT
1261 TTGTGGCCAT TTGCCACCCA TTGCGCCATG CTTCTGTGCT GACAGGGTGT ACTGTGGCCA
1321 AGATTGGACT ATCTGCCCTG ACCAGGGGGT TTGTATTCTT CTTCCCACTG CCCTTCATCC
1381 TCAAGTGGTT GTCCTACTGC CAAACACATA CTGTCACACA CTCCTTCTGT CTGCACCAAG
1441 ATATTATGAA GCTGTCCTGT ACTGACACCA GGGTCAATGT GGTTTATGGA CTCTTCATCA
1501 TCCTCTCAGT CATGGGTGTG GACTCTCTCT TCATTGGCTT CTCATATATC CTCATCCTGT
1561 GGGCTGTTTT GGAGCTGTCC TCTCGGAGGG CAGCACTCAA GGCTTTCAAC ACCTGCATCT
1621 CCCACCTCTG TGCTGTTCTG GTCTTCTATG TACCCCTCAT TGGGCTCTCG GTGGTGCATA
1681 GGCTGGGTGG TCCCACCTCC CTCCTCCATG TGGTTATGGC TAATACCTAC TTGCTGCTAC
1741 CACCTGTAGT CAACCCCTT GTCTATGGAG CCAAGACCAA AGAGATCTGT TCAAGGGTCC
1801 TCTGTATGTT CTCACAAGGT GGCAAGTGAG ACACCTTAGT GTCTCGCTTC TACTACTACT
1861 ACAGAAGATG GGAATATTAG GATCCTATTG AATGCCTTGG TGATTAAAGT ATCAAACCTA
1921 TTGTGCTGTC TTCTTCCAGC AATTTAAGTA GATCATGTAT TCTGTCTCCA GGAATGTGTC
1981 AGTACTGAAC TTATGACCCT GTCTGGACAT CCTGGAGAAT GACTGCACTA GTCCCTCTGC
2041 TATGGTGGTC TTGCCTTCTC CTTCTCTCTC AGCTAGAAAA TACATCTAGT TTTGACATGG
2101 GGAGGCTGTA AAGATCACAC CTCATGGTTC ATTCCAGTTT TGAAGTATGA TTTTAATGTT

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2161 CTTGCCCCCA TGTGCCCATG TTGGTGAATT TGCATGGACT ATAAACGTTA TTGCAAATAC
 2221 CCTAAAGTGG TTACCCAGCC ATAATCAGGG GTTAATGAAG GTATTTGGGG AATAGTAACT
 2281 GGAGAGACAG CAACAAGACA AGAGGCAGCT CACATGCAAT GTTGAAGTTT CTGTATGCAA
 2341 GAGGGTGTGT TGGCAGATTT GTGAAATCTG CCCATTTGCA TCTGTATGGC TCTATATGAC
 2401 TATTTGTCCA TAAGGGTGCC ATGTATTCTG GTTGTGGGTG TGAATGTGTG GGTGTGTTTA
 2461 TGTGGACACT TGCTTTTCAG TGTGCGTATA TGTGAGAGAG AGGGTGCACA CATGGAATAC
 2521 GTACTGGTTG TGTCTGGTG AGTGTGGTAG CTATGTCCTG GCACATGTAT GTTTCATGAG
 2581 ACGTGTCTCT GATTGCGCAT TTGTATTTCT GTGGTATCTG TTAGTTGGTA TATGATATGT
 2641 GTCTACGTGA GAATGCTGGT GTCTGTATCT GCATGGTGGG CAGTACCTTT ATGTGTATCT
 2701 GGTAAGAATG CTGCCTCTAC CTTTTCTTCC TATTTGTAAT ATGTGAATGT GGTGCATGAA
 2761 TGTGTGGAAT GTGTGGAATG TGTAAGTATT GGATGCCTGT ATCTTTCAGC GTGTTTGGGT
 2821 GTATGTCCAC TGTGCATAAT ATTTGAGATG TAAAACCATT TTGTGCGGTA TATGTGTTAT
 2881 TAGTTGTAAG TCGGTGAAAT GTACATCTGA ATTCTGTGTG CATATTGTTG GTACTGATGC
 2941 TATTTTCGTG CATATGTCTA GTGTATATGT TTTAAGGCAA ACTTTCCTTG TGTGTTGGGT
 3001 GTGTATGTGA CACGAATGGG GACAGCATCT GTATTTCTGA GCATGGATTG ATGTGTGGTG
 3061 TCTGTATGTA TCTTGGAATG GAGGAGGGAG ATTGAAGAAG TCTGGCTGTG AGCAGCAGAA
 3121 ATAATTTCCA AAGTTGAGTG ACATGACTCT AAGATGCCCA GTTTCCTCGG CTGGGGTCAG
 3181 CCTGGGTGAT AGCTCAGTCT GTCAGAATGA AAGGAAACAC GGTGCTTCCT TGCTCCACCT
 3241 TTTACAGGC CAGACCACAC CTTCTTCATC CTGAACACAA GGATTTCAAG GGCTTTTGTT
 3301 ACCTCTTCCT ACGTTTCCTG CCTCTGCTAT CCGAGGCACT GGCCTCCCTA AACCTGCCC
 3361 TCCTGCCTCA ATAGCAAGTC ATGGTATCCT CACCTCTCCC TTCCCTTTTT GGCTTATCTG
 3421 CCTAAACATGT ATAAAGTCC TTGGTTCCCC ATCTCTACTA AAAATACAAC AATTAGCCGG
 3481 GTGTGATGGC GCGTGCCTGT AGTCCCAGCT AGTTGGGAGG CTGAGGCAGG AGAAACGCTT
 3541 GAGCCCGCAA GGTGGAGGTT GCAGTGAGCC GAGATCATGC CACTGCACTC CAGCCTGGTG
 3601 ACAGAGCAAG ACTCTGTGTC AAAAAAAAAA AAAAAAAAAA AGCCTTGGTT GTAGGGAGTT
 3661 TCTCCTAATC CCTCTGGGAA AGCAAGGGTG GAGGGGAAGC CAGTCAATCT CCCTTCTGTT
 3721 GCCGCATGGA AACTCCCTTA AGGCAGGAAG CTGAAAAAAC TGTAGCATTC ACCTCATTAT
 3781 TCACCTTGTC TCATGTCTCA CTGTCCTTCC ACATGTCTCA TTGTTACTCC ATATTGGATG
 3841 GAAGTAGAAG TCCCTTTGGT ATTTTTTAAA GTCTTTGCCA TGTCTAAGTT AATGAGGTTA
 3901 ATGGAGGCAG CAGAGATGGC TCCAGGGTTC TGATAGCAAG TGTCAGGCTG CGTGCTCTGT
 3961 AGGCACCAGA AACTGTTGTC ACCAGTAATT TTGATGTGGT CTGAGTTAGA ATGGTCTGAT
 4021 TTGCCATGAT CTATTTAACA TAGCTTGATT TAGCGTGTCC TGTGTTCTGA ATTTAAACT
 4081 CACAGTTGTG AAACTGATCA GTAAAAAATA AGGGGAGACC AACTAAAAAC CATGTTGTTT
 4141 TATTTATAGA TGTAAGTTTT ACTTATTTCA AAATACGAGG TATTTAGTTT TACATTCAAA
 4201 TTGTTCTCTA ACTCTCTAAA ATGTTCTCTG ACTATTTTTG CCCTTAAGGG AGAAACCAGA
 4261 TGTCATTGGT CTTACGTGGC TGGTGTGGG GGTGGGGAGG GTTAAAGAAA CCACGTTCTC
 4321 TGTCCTCAGC CAGAAGTTCA GTAATCCAAG GCCAGAGAGT GGACGGCAGA GGCCTGTCC
 4381 CTGGGGACCT TGTTTATAAG TTATCCAAG ACAGGGACCA GAGCCTGGGA GACAAAAAAA
 4441 GATGTAGCCC TAGGGCTTTG GGAAAAGGAG GATGGACCCA GTGAATTCCA CGCTTAGCAA
 4501 GGACCTAAAC AGTGTCCCC AAATGAGAGA AGGGAGGACA GAAAGAACAC TTCAGGATGG
 4561 AAATGGGCTG AACTTAACC GTGGAGTGTC TCTGCAAACT TCCTTTGCCA TTCTCTGTT
 4621 TGAGTTTGAT AAACCTGAGA AGAGACTTGG ATAAAGACCG TCACGAAGAC TACACTAATG
 4681 AGTTTCTTCT AGCTTTTTTC TACTCACTTT CCCTATCTAT CCTTCACATT GGGAGTTGGC
 4741 ATGAGGATCC CAGCAGCCCA TCAGGGGAGG ACTCTAGAGA TCCCTTTCCC CATTCCTCT
 4801 CCTCCCCATA CCCCAGGCA TATCCTCCCA GGGCACGGAA GCTGAGAAGC AGTCCAGAAC
 4861 CACAGTGGGC TAGTGAGGGG TACCTGCTGA TGTACCCTTT GGACAGCATT CTGCCCCACC
 4921 CTGCAGGAAG AAGCAGAAGG AGGGAGAGGG TGAGGCAGAG AATAAATAAC CCTGACCAGG
 4981 GAGGTCCAAG GGAGTAGGCG GAGAcagaga ggctgtattt cagtgcagcc tgccagacct

Note: The three high score predictions of promoters were bold and underlined. The lower case sequence indicates the beginning part of the transcript of 101P3A11 gene.

Table XXX, beginning at page 214, line 35, has been amended as follows

Table XXX: Promoters and their positions predicted by Neural Network Promoter Prediction computer program (various portions of SEQ ID NO: 2867, respectively, in order of appearance).

Start	End	Score	Promoter Sequence
25	75	0.91	TTTTGCATTTTTTAATAGAGGCAGGGTTTCACCATGTTGGCCTGGCTGGTC
665	715	0.95	CAGGAAGTTGTATATAAGGAGAATCAGAGCAGAGAGAGACTAGGGTTCAG
2477	2527	0.91	TCAGTGTGCGTATATGTGAGAGAGAGGGTGCACACATGGAATACGTACTG
3139	3189	0.82	TGACATGACTCTAAGATGCCAGTTTCTCGGCCTGGGGTCAGCCTGGGTG
3420	3470	0.96	GCCAAACATGTATAAAAGTCCTTGGTTCCCATCTCTACTAAAAATACAA
4092	4142	0.99	AACTGATCAGTAAAAAATAAGGGGAGACCAACTAAAAACCATGTTGTTCT
4953	5003	0.97	AGGCAGAGAATAAATAACCCTGACCAGGGAGGTCCAAGGGAGTAGGCGGA

Table XXXI, beginning at page 215, line 1, has been amended as follows:

Table XXXI: Alignment of five homologous 5' upstream genomic regulatory regions of the human 101P3A11 and PSA genes.

Query: 5' upstream regulatory region of the PSA gene

Subject: Putative 5' upstream regulatory region of the 101P3A11 gene.

Nucleic acid sequences predicted to be binding sites for the indicated transcription factors are **bolded**, underlined, or *italicized*.

1. NF-1 SP-1 NF-1

Query: 3864 ccaggctggagtgcaagtggcgagctctcggtcactgcaacctctgcctcccaggttcaa 3923
(SEQ ID NO: 2868)

Sbjct: 3598 ccaggctggagtgcaagtggcatgatctcggtcactgcaacctccaccttgcggttcaa 3539
(SEQ ID NO: 2869)

Query: 3924 gtgattctcctgcctcagcctcctgagttgctgggattacaggcatgcagcaccatgccc 3983

Sbjct: 3538 gcgtttctcctgcctcagcctcccaactagctgggactacaggcacgcgccatcacaccc 3479

Query: 3984 agctaatttttgtatttttagtagagatgggg 4015

Sbjct: 3478 ggctaattgttgtatttttagtagagatgggg 3447

2.

Query: 4670 cctgtaatcccagctactgaggaggctgaggcaggagaatcacttgaacccagaaggcag 4729
(SEQ ID NO: 2870)

Sbjct: 3496 cctgtagtcccagctagttgggaggctgaggcaggagaacgcttgagcccgcaaggctgg 3555
(SEQ ID NO: 2871)

			SP1			NF-E	
			NF-1	NF-1		GR	GR
Query: 4730	aggttgcaatgagccgagattgcgccactgcactccagcctgggtgacagagtgcagctc	4789					
Sbjct: 3556	aggttgcaatgagccgagattgcgccactgcactccagcct-ggtgacagagcaagctc	3614					

Query: 4790 tgtctcaaaaaaaaaa 4807

Sbjct: 3615 tgtctcaaaaaaaaaa 3632

